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RESEARCH PTY. LIMITED filed on 29 August 1997.

I further certify that the annexed specification is not, as yet, open to public inspection.

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A handwritten signature in cursive script, appearing to read 'Kim Marshall'.

KIM MARSHALL
MANAGER EXAMINATION SUPPORT AND
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AUSTRALIA

PATENTS ACT 1990

PROVISIONAL SPECIFICATION

FOR THE INVENTION ENTITLED:-

"CYTOCHROME P450 REDUCTASE FROM POPPY PLANTS"

The invention is described in the following statement:-

TECHNICAL FIELD

The present invention relates to production of alkaloids from poppy plants and in particular to genes encoding enzymes in the alkaloid pathway, to proteins encoded by the genes and to methods of increasing alkaloid content of poppy plants.

5

INTRODUCTION

The opium poppy *Papaver somniferum* is grown under strict government control, for the production of medically useful alkaloids such as morphine and codeine. The alkaloid content of poppy straw (includes threshed poppy capsules) is the most important parameter in the efficiency of opium alkaloid production. There have been numerous attempts to increase the yield of alkaloid per ton of poppy material. The vast majority of approaches focus on improving agricultural practices and on established methods of conventional breeding in the attempt to increase cultivation efficiencies and to modifying the genotype of the opium poppy plants.

In addition to increasing the overall yield of opium alkaloids, the relative content of particular alkaloids in the poppy plants is also of considerable importance and has an impact on efficiency of processing of the plant material and the ultimate yield and cost of an alkaloid.

Usually only one of the many alkaloids that can be produced by a poppy plant is found as the predominant alkaloid. In the opium poppy this is predominantly morphine which accumulates after flowering of the plant. However, before flowering thebaine is most abundant. The reason for such bias can be explained, at least in part, by analysis of what is currently known about alkaloid metabolism in the opium poppy and its regulation.

The network of reactions, enzymes, co-factors and metabolic intermediates leading to the synthesis of alkaloids in the opium poppy constitute a complex metabolic pathway which is regulated at numerous points. There are also thought to be a number of rate limiting steps ("bottlenecks") where limitations in the availability of either substrates, co-factors or certain enzymes, determine which particular branch of the synthetic pathway is favoured and therefore the ultimate "mix" of alkaloids and the type of alkaloid which is predominantly in the plant. A class of enzymes known as cytochrome P-450 are known to be involved in the synthesis of several intermediates in the pathway. However, unlike the enzymology of mammalian cytochrome P450

enzymes, similar plant enzymes are considerably less abundant (Biochimie 1987, 69:743-752) and have been less clearly described. It is known that plant P450 enzymes are like mammalian proteins and that they are hemoproteins which have a common prosthetic group containing iron and are membrane-bound proteins found within the endoplasmic reticulum. Generally, the P450-dependent enzymes catalyse the transferral of oxygen to the substrate and effectively remove one of the atoms from an oxygen molecule and are also referred to as monooxygenases. The reactions are dependent on a range of co-factors including NADPH and a second enzyme P450 cytochrome reductase.

More particularly, in the biosynthesis of alkaloids in plants, cytochrome P-450-dependent oxidases and monooxygenases have been shown to catalyse highly regio- and stereoselective reactions. Hydroxylases and oxidases specific to alkaloid biosynthesis have been identified and characterised for the protopine, berberine, bisbenzylisoquinoline, benzophenanthridine, morphinan and monoterpenoid indole alkaloid biosynthetic pathways. The role of cytochrome P-450s in alkaloid biosynthesis is exemplified by the biosynthesis of sanguinarine in *Eschscholzia californica* (California poppy). Of the six oxidative transformations involved in the conversion of (*S*)-reticuline to sanguinarine, four are thought to be catalysed by cytochrome P-450-dependent enzymes.

Thus, plant cytochrome P-450-dependent enzymes, including those from the alkaloid poppy, constitute a substrate-specific class of enzymes that differs from their mammalian counterpart in the high regio- and stereospecificity as well as in the novel nature of the reactions catalysed. The enzymes involved in the alkaloid biosynthetic pathway require among other things the presence of a cytochrome P-450 reductase enzyme. Plant cytochrome P-450 reductases have been purified or enriched from *C. roseus* (1, 8), sweet potato (9), *Helianthus tuberosus* (Jerusalem artichoke) (10), *Glycine max* (soybean) cell suspension cultures (11), *Pueraria lobata* (12) and petunia flowers (13). cDNA encoding cytochrome P-450 reductase has been isolated from *Vigna radiata* (mung bean) (14), *C. roseus* (15), *H. tuberosus* (accession Z26250, Z26251), *Vicia sativa* (accession Z26252) and *Arabidopsis* (16). cDNA cloning and heterologous expression in *E. coli* of the *C. roseus* cytochrome P-450 reductase has been reported (15).

The reductase is responsible for providing electrons to the P450 and is thought to be a relatively promiscuous enzyme in that a particular reductase species will reduce a range of distinct P450s. It is also known that the cytochrome P450 enzymes are in molar excess to the level of P450 reductase. This imbalance may be a regulatory step for the reduction and therefore be rate-limiting of the cytochrome P450 activity. Although there is some promiscuity within species, available data suggests that there is poor transferability of reductases from diverged species. For example, although cytochrome P-450 reductase from insect cell culture and porcine liver was shown to transfer electrons to heterologously expressed *Berberis* berbaminine synthase, the highest turnover number was achieved with the *Berberis* reductase (7).

Notwithstanding this body of work, to date it has not been possible to establish the exact nature of the "bottlenecks" in the alkaloid metabolism pathway or to identify the key enzymes which may be responsible and which could be used to manipulate alkaloid metabolism in the opium poppy in order to achieve higher yields of alkaloids generally, and specific alkaloids in particular.

As the cost of producing poppy alkaloids is very dependent on the alkaloid content of poppy straw, it would be a major advantage if high alkaloid containing straw could be obtained rather than to attempt to increase the yield of straw. In fact, it is possible that any increase in the yield of straw may result in the relative content of alkaloid decreasing through dilution. High alkaloid-containing straw would provide efficiencies throughout the CPS ("Concentrate of Poppy Straw") production process. If high crop yields can be achieved, either less hectares of crop need be grown or the pre-existing areas can be used to increase production. High yield crops would also reduce the cost of harvest, transport, drying, storage, processing and waste disposal per unit weight of alkaloid. Thus, to increase the yield of an alkaloid it would be most efficient to manipulate the plants to increase alkaloid content of the straw rather than to increase the yield of straw.

SUMMARY OF THE INVENTION

It has now been found that among the rate-limiting steps in the production of morphine in *Papaver somniferum* are the steps which depend on the cytochrome P-450 enzymes, and therefore in turn on the cytochrome P-450 reductases. This observation has led to the identification and isolation of cytochrome P-450 reductase enzymes in the

alkaloid poppy, the isolation and characterisation of polynucleotides encoding the reductase enzymes, the expression of the polynucleotides encoding the reductases in eukaryotic and prokaryotic expression systems, including plant cells and transfected or transformed plants. The identification of cytochrome P-450 reductase genes and their products in poppy plants now enables methods of controlling the total alkaloid content of a plant, the ultimate "mix" of alkaloids as well as the type of predominant alkaloid synthesised by the plant. This can be achieved by alleviating the "bottlenecks" in the pathway through overexpression of the relevant reductase genes in plants transformed or transfected with a nucleotide sequence encoding an appropriate P-450 reductase enzyme.

Thus, according to a first aspect there is provided an isolated and purified polynucleotide encoding a cytochrome P-450 reductase enzyme from an alkaloid poppy plant, or a variant or fragment thereof.

The polynucleotide may be selected from the group consisting of genomic DNA (gDNA), cDNA, or synthetic DNA. The preferred polynucleotides encoding a cytochrome P-450 reductase are selected from those shown in Figures 9a and 9b or fragments thereof. It will be understood however that sequences shown in the Figures 9a and 9b may be expressed in the absence of the native leader sequences or any of the 5' or 3' untranslated regions of the polynucleotide. Such regions of the polynucleotide may be replaced with exogenous control/regulatory sequences in order to optimise/enhance expression of the sequence in an expression system. Figures 10a and 10b represent examples of truncated polynucleotide sequences encoding cytochrome P-450 reductases of *P. somniferum* and *E. californica* respectively, wherein the native leader sequences have been removed in order to enhance the expression of the enzyme.

The preferred alkaloid-producing poppy plants are *Eschscholzia californica* and *Papaver somniferum*.

It will also be understood that analogues and variants of the polynucleotide encoding a cytochrome P-450 reductase from alkaloid poppy plants fall within the scope of the present invention. Such variants will still encode an enzyme with cytochrome P-450 reductase properties and may include codon substitutions or modifications which do not alter the amino acid encoded by the codon but which enable efficient expression of the polynucleotide encoding cytochrome P-450 reductase enzyme in a chosen expression

system. Other variants may be naturally occurring, for example allelic variants or isoforms.

According to a second aspect there is provided an isolated and purified polynucleotide which binds under stringent conditions to the nucleotide sequence
5 encoding a cytochrome P-450 reductase enzyme from an alkaloid poppy plant, or a fragment thereof.

Such complementary polynucleotides are useful in the present invention as probes and primers, as antisense agents or may be used in the design of other suppressive agents such as ribozymes and the like.

10 According to a third aspect there is provided an isolated and purified polynucleotide which codes for prokaryotic or eukaryotic expression of a cytochrome P-450 reductase enzyme from an alkaloid poppy plant, or a variant or fragment thereof, wherein the polynucleotide is expressed in an environment selected from the group consisting of the extracellular environment, an intracellular membranous compartment,
15 intracellular cytoplasmic compartment or combinations thereof.

The polynucleotide encoding a cytochrome P-450 reductase may be coupled to another nucleotide sequence which would assist or directing the expression of the reductase with respect to a particular cellular compartment or the extracellular environment.

20 According to a fourth aspect there is provided an isolated and purified cytochrome P-450 reductase enzyme from an alkaloid poppy plant, being a product of prokaryotic or eukaryotic expression of the polynucleotide of the first aspect or the second aspect.

Variants of the cytochrome P-450 reductase enzyme which incorporate amino
25 acid deletions, substitutions, additions or combinations thereof, are also contemplated. The variants can be advantageously prepared by introducing appropriate codon mutations, deletions, insertions or combinations thereof, into the polynucleotide encoding the P-450 reductase enzyme. Such variants will retain the properties of the P-450 reductase enzyme, either *in vivo* or *in vitro*. Other variants may be naturally
30 occurring, for example allelic variants or isoforms.

The cytochrome P-450 reductase may be expressed in and by a variety of eukaryotic and prokaryotic cells and organisms, including bacteria, yeasts, insect cells,

mammalian and other vertebrate cells, or plant cells. Preferably the expression system is a plant expression system and even more preferred is an alkaloid poppy plant. Suitable alkaloid poppy plants are *Eschscholzia californica* and *Papaver somniferum*.

For expression of cytochrome P-450 reductase activity, a fragment of the polynucleotide encoding a cytochrome P-450 reductase may be employed, such fragment encodes functionally relevant regions, motifs or domains of the reductase protein. Similarly, fragments of the P-450 reductase enzyme resulting from the recombinant expression of the polynucleotide may be used. Functionally important domains of cytochrome P-450 reductase may be represented by individual exons or may be identified as being highly conserved regions of the protein molecule. Those parts of the cytochrome P-450 reductase which are not highly conserved may have important functional properties in a particular expression system.

According to a fifth aspect there is provided a method for preparing plants which overexpress a cytochrome P-450 reductase enzyme, comprising transfecting or transforming a plant cell, a plant part or a plant with the polynucleotide according to the first aspect or the second aspect.

Preferably, the plants overexpressing the P-450 reductase are *Eschscholzia californica* and *Papaver somniferum*. Suitable promoters to control the expression of the P-450 reductase gene may be derived from for example cauliflower mosaic virus or subterranean clover mosaic virus. Other virus promoters may also be suitable. Further, the use of the endogenous promoter may also be appropriate in certain circumstances. Such a promoter may be co-isolated with the gDNA encoding the P-450 reductase enzyme.

According to a sixth aspect there is provided a cell transformed or transfected with a polynucleotide of the first aspect or the second aspect.

Cells which may be transfected or transformed with a polynucleotide encoding a cytochrome P-450 reductase are bacterial, yeast, animal or plant cells. For preference the cells are plant cells. Even more preferred are cells from an alkaloid poppy plant, such as *Eschscholzia californica* or *Papaver somniferum*.

According to a seventh aspect there is provided a plant transformed or transfected with a polynucleotide according to the first aspect or the second aspect, wherein the plant exhibits modified expression of the cytochrome P-450 reductase enzyme.

For preference, the modified expression manifests itself in overexpression of the cytochrome P-450 reductase enzyme. However, reduced expression of cytochrome P-450 reductase can also be achieved if the plant is transformed or transfected with a polynucleotide which is complementary to the polynucleotide encoding the reductase.

5 According to a eighth aspect there is provided an alkaloid poppy plant transformed or transfected with a polynucleotide according to the first aspect or the second aspect, wherein the plant has a higher or different alkaloid content when compared to a plant which has not been so transformed or transfected.

Preferably the plants expressing higher alkaloid content are selected from
10 *Eschscholzia californica* and *Papaver somniferum*. Even more preferred is *Papaver somniferum*.

According to a ninth aspect there is provided a recombinant DNA molecule comprising the polynucleotide according to the first aspect or the second aspect.

Preferably the recombinant DNA molecule is a viral or plasmid vector. Such a
15 vector may direct prokaryotic or eukaryotic expression of the polynucleotide encoding a cytochrome P-450 reductase or it may prevent or reduce its expression.

According to a tenth aspect there is provided a method of altering the yield or nature of alkaloid in a plant comprising transforming or transfecting a plant with a polynucleotide encoding a cytochrome P-450 reductase enzyme or a variant or fragment
20 thereof, or with a polynucleotide which binds under stringent conditions to the polynucleotide encoding said enzyme.

According to a eleventh aspect there is provided a method of increasing the yield of alkaloid in a plant comprising transforming or transfecting a plant with a polynucleotide encoding a cytochrome P-450 reductase enzyme or a variant or fragment
25 thereof, wherein the enzyme is overexpressed in said plant.

According to a twelfth aspect there is provided a method of altering type or blend of alkaloid in a plant comprising transforming or transfecting a plant with a with a polynucleotide encoding a cytochrome P-450 reductase enzyme or a variant or fragment thereof, or with a polynucleotide which binds under stringent conditions to the
30 polynucleotide encoding said enzyme.

For preference the alkaloid is morphine, codeine, oripavine or thebaine, but it will be understood that other intermediates in the alkaloid metabolic pathway are also within the scope of the present invention.

BRIEF DESCRIPTION OF FIGURES

5 **Figure 1.** SDS-PAGE analysis of fractions from the purification of cytochrome P-450 reductase from *P. somniferum* cell suspension cultures. Protein bands were visualized by silver staining. Lane 1, protein standards; lane 2, affinity chromatography elution buffer without protein; lane 3, 1 μ g protein from the 2',5'-ADP Sepharose 4B eluate after dialysis; lane 4, 4 μ g microsomal protein; lanes 5,6, 4 μ g solubilized
10 microsomal protein; lane 7, 4 μ g protein from the DEAE cellulose eluate.

Figure 2. Amino acid sequences of seven endoproteinase Lys-C-generated peptides of the cytochrome P-450 reductase from *P. somniferum* cell suspension cultures.

Figure 3. Partial amino acid sequence comparison of plant cytochrome P-450 reductases. The shaded areas and arrows indicate the position and direction of the
15 regions used for PCR oligodeoxynucleotide primer design.

Figure 4. Genomic DNA gel blot analysis of (A) *P. somniferum* hybridized to the *P. somniferum* full-length cDNA and (B) *E. californica* hybridized to the *E. californica* full-length cDNA and to (C) the 288 bp PCR fragment corresponding to the second isoform. The numbers following the restriction enzyme names indicate the number of
20 recognition sites that occur in the reading frame. For the second *E. californica* isoform, this is known only over a 288 bp region.

Figure 5. Comparison of the amino acid sequences of the cytochrome P-450 reductase from *P. somniferum* and from *E. californica*. Top sequence, *E. californica*; bottom sequence, *P. somniferum*; *, amino acid identity.

25 **Figure 6.** Nucleotide sequences of cDNA from (a) *P. somniferum*, and (b) *E. californica*.

Figure 7. Functional expression of cytochrome P-450 reductases in yeast and insect cell culture. (A) Expression of pYES2/PsoCPRI (———), pRS405/PsoCPRII (— - —), pYES2/PsoCP (.....), control (.....); (B) pFastBac/PsoCPRII (———), control (.....); (C) pYES2/EcaCPRII (———), pRS405/EcaCPRII
30 (———), control (.....);

(— - —), control (.....); (D) pFastBac/EcaCPRII (———), control (.....). Pso CPR, *P. somniferum* cytochrome P-450 reductase; Eca CPR, *E. californica* cytochrome P-450 reductase; Sf9, *S. frugiperda* Sf9 cell culture.

Figure 8. Restriction enzyme map (unique sites) for cDNA sequences of (a) *P. somniferum*, and (b) *E. californica*.

Figure 9. Amino acid sequences of (a) *P. somniferum*, and (b) *E. californica*, predicted from their respective cDNA nucleotide sequences. The start and stop codons are depicted in bold.

Figure 10. cDNA nucleotide sequences and their predicted amino acid sequences, of fragments subcloned into an expression vector: (a) *P. somniferum*, and (b) *E. californica*. Both sequences are truncated versions of sequences represented in Figures 9a and 9b, lacking the leader sequences. Extra vector sequences/restriction sites derived during subcloning are shown in lowercase and the cDNA in uppercase.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

The details of the metabolic pathway leading to synthesis of opium alkaloids in the opium poppy, *Papaver somniferum*, part of which is depicted in Scheme I. Typically, the P450 enzyme exists in a 15 - 20 fold excess as compared to the reductase level and as there is approximately a 6:1 dependence between the two enzymes, it is feasible that the reductase levels are limiting the rate of the cytochrome P450 enzyme. By supplying plant tissue with radiolabeled compounds and following the accumulation of radioactivity in the various intermediates in the pathway it was shown that addition of radiolabel (labeled reticuline, salutaridinol) before thebaine results in accumulation of radioactivity at thebaine. Addition of radiolabeled compounds after thebaine result in the accumulation of radioactivity at codeine.

Oripavine is an intermediate from a second route of conversion from thebaine to morphine. It is thought that thebaine is converted to oripivine by the same 3 demethylase that converts codeine to morphinone. The slow modification of the isotopic oripavine is probably due to the rate limitation of the 6 demethylase.

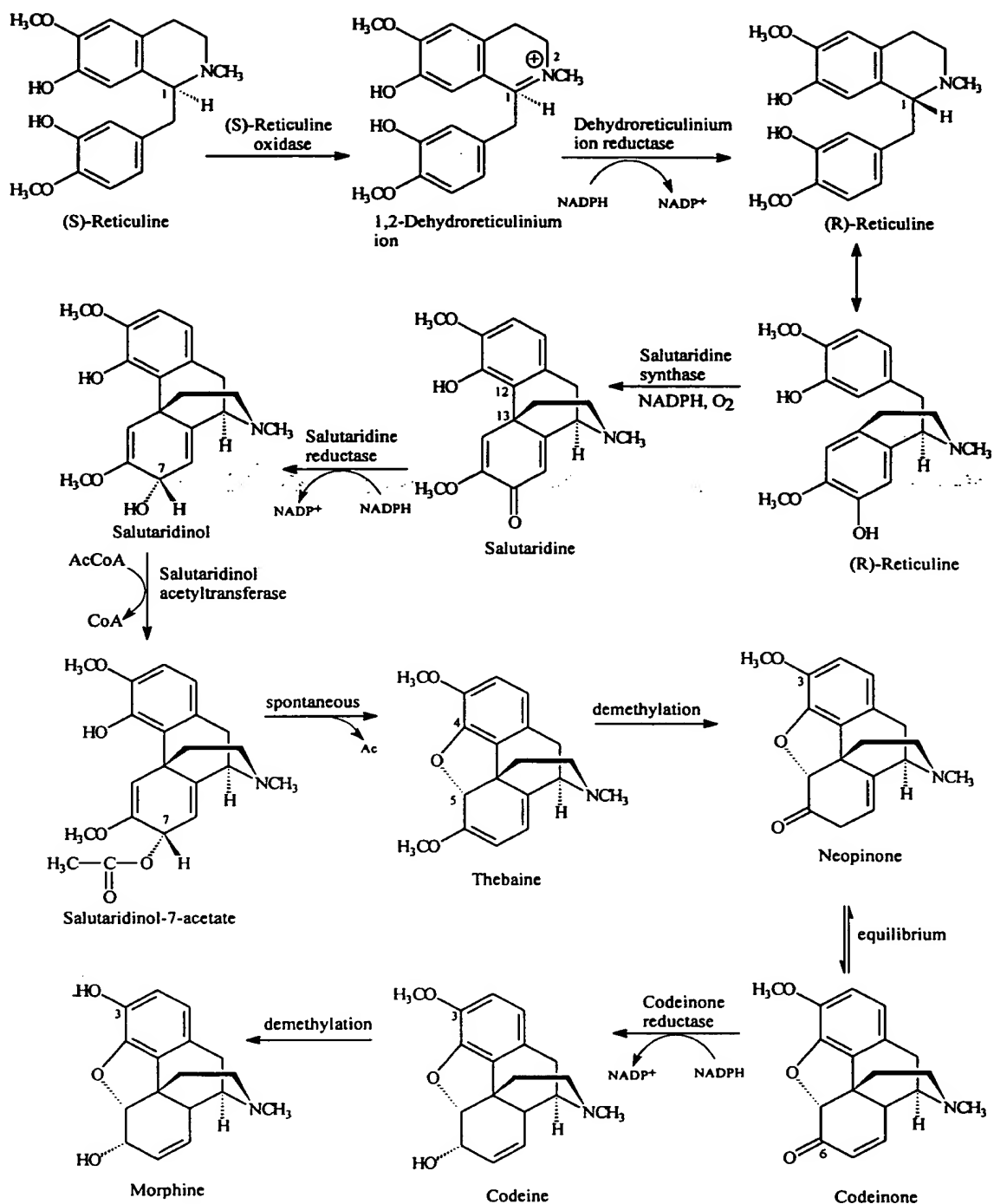
With the assistance of such experiments it has now been found that among the rate-limiting steps in the production of morphine in *Papaver somniferum* are the steps

which depend on the reduction of cytochrome P-450 by the cytochrome P-450 reductases.

Thus the following steps are known or suspected to be catalysed by P-450 enzymes which are rate limiting:

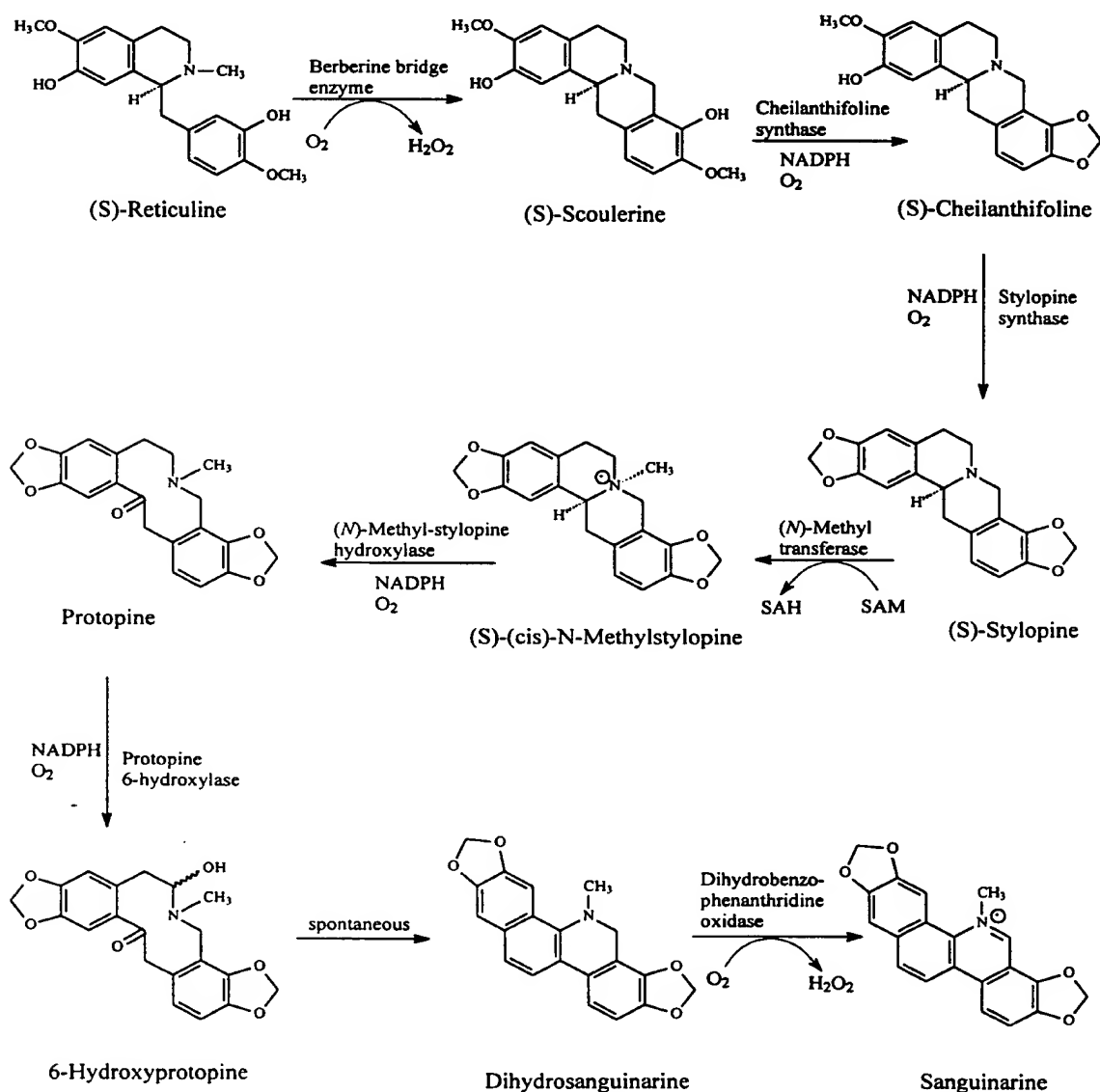
- 5 1 (R)-reticuline → salutaridine
- 2 thebaine → neopinone → codeinone
- 3 codeine → morphine

- 12 -
SCHEME I



The importance of cytochrome P-450 in alkaloid biosynthesis is also exemplified by the biosynthesis of sanguinarine in *Eschscholzia californica* (California poppy). This biosynthetic pathway is shown in Scheme II.

SCHEME II



The present invention provides by way of example the sequence of the P-450 reductase enzyme genes from two poppy species, the opium poppy *Papaver somniferum* and the Californian poppy *Eschscholzia californica*. The sequence information has been shown to code for the enzymes by expression in a heterologous expression system
5 followed by biochemical characterisation. These studies have also shown that the alteration of the ratio and species of reductase will significantly alter the interaction of the cytochrome P-450 with its substrate suggesting a lack of tolerance for general interchange of reductase genes.

The over-expression of the P-450 reductase gene in an alkaloid producing plant
10 will alleviate the rate-limitation of the P450 by increasing the rate of reduction of the active P-450 enzyme. In brief, controlling the reductase should control the P-450 cytochrome.

The information on the protein coding region of cytochrome P-450 reductase enzymes may be applied to increase yields of alkaloids in the poppy plant as follows:

- 15 1) obtain the gDNA or cDNA sequence of the gene from the target plant and a closely related plant.
- 2) sub-clone the gDNA or cDNA into a plasmid vector that contains the following:
 - a promoter suitable for overexpression of the cDNA in poppy, for example a promoter derived from the cauliflower mosaic virus or the subterranean clover
20 mosaic virus.
 - a selectable marker linked to a different promoter to facilitate the selection of transformants. Marker could be a dominant marker such as a herbicide resistance gene or an antibiotic resistance gene.
 - suitable selectable markers and replication origins for maintenance of the
25 plasmid in bacteria
 - suitable sequences to facilitate mobilisation of the plasmid by *Agrobacterium tumefaciens*-mediated transformation.
- 3) transform a suitable strain of *A. tumefaciens* and then co-cultivate the bacteria with suitable samples of plant tissue such as callus, embryonic tissue or hypocotyl tissue.
- 30 4) place treated tissue on selectable media and provide appropriate media to promote differentiation and plant re-generation.

- 5) characterise candidate plants by Southern and Northern blotting to confirm integration of gene and expression in appropriate tissues
- 6) self-pollinate transformed plants, analyse segregants to identify hemizygotes and homozygotes
- 5 7) analyse biochemistry of transgenic plants.

Isotope labelling can be used to identify bottlenecks and HPLC analysis will determine levels of alkaloids.

In order to develop optimised convenient heterologous expression systems for the cytochrome P-450-dependent oxidases of select isoquinoline alkaloid-producing plant
10 species, facile PCR-based method have been developed with which to clone cytochrome P-450 reductase and express the enzyme in yeast and insect cell culture as initial expression systems.

The invention will now be described with reference to specific examples.

EXAMPLES

15 Example 1: Enzyme purification and amino acid sequencing:

Plant cell cultures. Cell suspension cultures of *P. somniferum* and *E. californica* were routinely grown in 1-litre conical flasks containing 400 ml of Linsmaier-Skoog medium (17) over 7 days at 23°C on a gyratory shaker (100 rpm) in diffuse light (750 lux). Elicitation of *E. californica* cell suspension cultures was achieved by the aseptic
20 addition of methyl jasmonate to a final concentration of 100 µM to the medium (18).

Purification and sequence analysis. Cells were harvested from seven-day-old suspension cultures of *P. somniferum* by vacuum filtration, immediately shock frozen and stored at -20°C. All of the following operations were carried out at 4°C. 500 g frozen tissue were then homogenized with a mortar and pestle in 1 litre 0.1 M
25 tricine/NaOH, pH 7.5 containing 15 mM thioglycolic acid. Cell debris was removed by centrifugation at 10,000 x g, 30 min. The supernatant was filtered through four layers of cheesecloth and the microsomes were then isolated by MgCl₂ precipitation according to (19). In a typical preparation, 500 g fresh weight of cells yielded 8-10 mg/ml
30 microsomal protein. Microsomal protein was solubilized as follows. 2 mg CHAPS (3-[(3-cholamidopropyl)dimethyl-ammonio]-1-propane-sulfonate, Roth) per mg microsomal protein was prepared in 1 ml of 0.1 M tricine/NaOH, pH 7.5 containing 15

mM thioglycolic acid. This solution was added dropwise to the microsomal suspension. 2% (v/v) Emulgen 911 (Kao Corporation) was then added and the solution slowly stirred for 1 h. Membrane fragments were removed by centrifugation at 105,000 x g for 60 min. The total activity in the solubilized microsomes was assigned the value 100%. The solubilized cytochrome P-450 reductase was then purified to electrophoretic homogeneity according to (20). In this manner, 50 µg cytochrome P-450 reductase was purified from 8 kg *P. somniferum* cell suspension culture in 97% yield.

The purified enzyme preparation was subjected to SDS/PAGE to remove traces of Emulgen 911 and CHAPS, and the coomassie brilliant blue R-250-visualized band representing the cytochrome P-450 reductase was digested *in situ* with endoproteinase Lys- C as reported in (21). The peptide mixture thereby obtained was resolved by reversed phase HPLC [column, Merck Lichrospher RP18; 5 µm (4 x 125 mm); solvent system, (A) 0.1% trifluoroacetic acid, (B) 0.1% trifluoroacetic acid / 60% acetonitrile; gradient of 1% per min; flow rate of 1ml/min] with detection at 206 nm. The scheme for the purification of the cytochrome P-450 reductase is given in Table I.

TABLE I Purification of Cytochrome P-450 Reductase from *P. somniferum* Cell Suspension Cultures

Purification Step	Total protein (mg)	Total activity (nkatal)	Specific activity (nkatal/mg)	Purification factor (fold)	Yield (%)
Microsomes	308	59	0.2	-	-
Solubilized microsomes	244	71	0.3	1	100
DEAE Cellulose	21	71	3.4	11	100
2',5'-ADP Sepharose 4B	0.05	47	927	3100	66
Dialysis	0.05	69	1385	4600	97

Following this facile purification procedure (20), 50 µg of enzyme could be purified to near electrophoretic homogeneity from 8 kg fresh weight of cell suspension culture with minimal loss of activity. Gel electrophoretic analysis of aliquots of the purification steps suggest that there may be two isoforms of the cytochrome P-450 reductase in *P. somniferum* as there were two protein bands present in the 2',5'-ADP

Sephacrose 4B eluate at 80 kDa (Fig. 1). To further test the possible presence of isoforms, 10 µg protein from the 2',5'-ADP Sepharose 4B eluate was subjected to native polyacrylamide gel electrophoresis, the two closely migrating protein bands were eluted and both tested positive for cytochrome *c* reduction. These two isozymes could not be chromatographically resolved and were therefore characterized together.

The purified reductase exhibited a pH optimum at 8.0 in 0.5 M Tricine buffer. The optimal molarity range of the Tricine buffer was determined to be 250-500 mM. At 100 mM and at 1 M Tricine, the activity declined to 21% and 77%, respectively. The K_m value for cytochrome *c* was 8.3 µM and that for the cofactor NADPH was 4.2 µM. The distribution of the cytochrome P-450 reductase in a 3-month-old *P. somniferum* plant is given in Table II.

TABLE II Distribution of Cytochrome P-450 Reductase Activity in a 3-Month-Old *P. somniferum* Plant

Plant part	Specific activity (pkatal/g dry weight)	Specific activity (pkatal/mg protein)
Capsule	2700	660
stem	2000	930
Leaf	840	390
Root	670	740

On a dry weight basis, the highest activity is present in the capsule.

Microsequencing was accomplished with an Applied Biosystems model 470 gas-phase sequencer. The amino acid sequence of seven endoproteinase Lys-C-generated peptides was determined on the mixture of both isozymes (Fig. 2). A comparison of these amino acid sequences with those available for plant cytochrome P-450 reductases in the GenBank/EMBL sequence database allowed the relative positioning of the seven internal peptides due to high sequence homology. This also served as supportive evidence that the isozymes that were purified were indeed cytochrome P-450 reductases.

Example 2: Generation of partial cDNAs from *P. somniferum* and *E. californica*.

Optimized PCR primers were then designed based on highly homologous sites on both the amino acid and nucleotide levels in the plant cytochrome P-450 reductase sequence comparison (Fig. 3). The precise sequence of the primers used for the first round of PCR was:

5'-CA ITI CII CCT CCT TTC CC-3' and
T

3'-ACC TAC TTC TTA CGI CAA GG-5'.
C TGC

5 Polymerase chain reaction (PCR) generated partial cDNAs encoding cytochrome P-450 reductases from *P. somniferum* and *E. californica* were produced by PCR using cDNA produced by reverse transcription of total RNA isolated from 3 to 5-day-old suspension cultured cells. DNA amplification was performed under the following conditions: 5 cycles of 94°C, 30 sec; 45°C, 1 min; 72°C, 1 min; 25 cycles of 94°C, 30
10 sec; 55°C, 30 sec, 72°C, 1 min. At the end of 30 cycles, the reaction mixtures were incubated for an additional 5 min at 72°C prior to cooling to 4°C. The amplified DNA was then resolved by agarose gel electrophoresis, the bands of approximately the correct size were isolated and subcloned into pGEM-T (Promega) prior to nucleotide sequence determination.

15 Resolution of this first PCR experiment by agarose gel electrophoresis revealed a mixture of DNA products in the expected range of 400-450 bp. The bands in this size range were eluted from the gel and used as template for nested PCR with the following primers:

20 5'-CA ITI CII CCT CCT TTC CC-3' and
T

3'-AAA CGI CGI TAI CGI GGI GCI IGI GTT GG-5'
G C

The result from the nested PCR was a single DNA band with the expected size of 288 bp. The translation of the nucleotide sequence of this PCR product indicated that it
25 was indeed encoding a cytochrome P-450 reductase. This 288 bp PCR-generated partial cDNA was then used as hybridization probe to screen an amplified *P. somniferum* cell suspension culture cDNA library. In this manner, from a total of 300,000 clones screened, two positive clones were isolated. Of these two positive clones, one was determine to be full-length by a restriction endonuclease analysis. The nucleotide
30 sequence of this full-length cDNA clone was then determined for both strands. The

reading frame coded for 684 amino acids corresponding to a relative molecular mass of 77.5 kDa.

An identical PCR-based approach was also carried out with RNA isolated from methyl jasmonate-induced *E. californica* cell suspension cultures (26). Nucleotide sequence determination of the 288 bp DNA fragment indicated that in *E. californica* one cytochrome P-450 reductase form is present. However, screening of 400,000 clones of a primary cDNA library prepared from RNA isolated from methyl jasmonate-induced *E. californica* cell suspension cultures resulted in the isolation of one partial and one full-length clone, both of which encoded a second isoform. The nucleotide sequence of this full-length cDNA clone was then determined for both strands. The reading frame encoded 705 amino acids that corresponded to a relative molecular mass of 78.7 kDa. RNA gel blot analysis indicated that this isoform gene is weakly induced two-fold by treatment of the cell cultures with methyl jasmonate. Genomic DNA gel blot analysis of each reductase indicates that one gene encodes each isoform in *E. californica* and that one gene also encodes the cloned isoform in *P. somniferum* (Fig. 4).

The overall sequence homology of the cytochrome P-450 reductase from *P. somniferum* and that from *E. californica* is 63% identity at the nucleotide level and 69% identity at the amino acid level (Fig. 5). This compares to an overall sequence identity to other plant cytochrome P-450 reductases of approximately 50% at both the nucleotide and amino acid levels.

Nucleotide sequence determination. The entire nucleotide sequence on both DNA strands of full-length cDNA clones in pBluescript was determined by dideoxy cycle sequencing using internal DNA sequences for the design of deoxyoligonucleotides as sequencing primers. Nucleotide sequences of cDNAs of *P. somniferum* and *E. californica* are given in Figures 6A and 6B, respectively.

Alternative approaches. cDNA can also be prepared by isolating RNA from either plant cell suspension cultures or from different material, according to a method using LiCl precipitation of ribonucleic acid as described in "Current Protocols in Molecular Biology" Ausubel FM, Brent R, Kingston RE, Moore DD, Seidman JG, Smith JA, Struhl K, eds John Wiley & Sons, Inc. New York (1987). mRNA was then isolated from the total RNA using either an oligo dT cellulose column or oligo dT beads (Oligotex beads, QIAGEN) according to the manufacturers instructions. The cDNA

libraries were prepared from mRNA with cDNA and lambda ZAP kits from Stratagen (La Jolla, California, USA), according to the manufacturers instructions.

Example 3: cDNA isolation and heterologous expression of cytochrome P-450 reductase in *Saccharomyces cerevisiae*.

5 cDNA clones encoding the *Papaver* and *Eschscholzia* cytochrome P-450 reductases were isolated by screening of cDNA libraries prepared in either λ -ZAP II or Uni-ZAP XR (Stratagene) using the partial clones generated by PCR as hybridization probe. The clones that yielded positive results through a third screening were converted to pBluescript KS (+) by excision. After determination of the nucleotide sequence on
10 both strands, the full length reading frame, free of the 5'- and 3'-flanking sequences, was generated by PCR using either *Taq* DNA polymerase (Perkin Elmer) and was subcloned into pGEM-T (Promega) or *Pfu* DNA polymerase and was subcloned into pCR-Script SK (+) (Stratagene).

The *P. somniferum* cytochrome P-450 reductase cDNA in pGEM-T, designated
15 pGEM-T/PsoCPR, was digested with the restriction endonucleases *Not* I and *Hin* dIII and the 2096 bp fragment was ligated into *Not* I/*Hin* dIII digested pYES2 (autonomously replicating yeast expression vector from Invitrogen) to produce the expression plasmid pYES2/PsoCPRI. This particular construction had 27 bp of a noncoding region upstream from the AUG start codon. This was reduced to 6 bp by digestion of
20 pYES2/PsoCPRI with *Hin* dIII and *Cla* I. This 55 bp restriction fragment was then replaced by ligation with a synthetic DNA adaptor of a sequence that replaced the reading frame from the internal *Cla* I site through the start codon, which was immediately preceded by a *Hin* dIII recognition sequence. The resulting construct was termed pYES2/PsoCPRII.

25 The *E. californica* cytochrome P-450 reductase cDNA in pGEM-T, designated pGEM-T/EcaCPR, was digested with the restriction endonucleases *Sal* I and *Not* I and the 2289 bp fragment was ligated into *Sal* I/*Not* I digested pGEM-9Zf (-) (Promega). pGEM-9Zf/EcaCPR was then digested with *Sst* I and *Not* I and the 2292 bp fragment was ligated into *Sst* I/*Not* I digested pYES2 to produce the expression plasmid
30 pYES2/EcaCPRI. The noncoding sequences upstream of the start codon were minimized by digestion with *Sma* I and *Eco* ICRI and the vector recircularized by blunt-

end ligation (plasmid termed pYES2/EcaCPRII). These autonomously replicating expression plasmids were then introduced into the *Saccharomyces cerevisiae* strain INVSC1 under uracil selection.

5 Expression of the vector pYES2/PsoCPRII containing 27 noncoding nucleotides upstream of the start codon resulted in increased enzyme activity that was 2.6-fold greater than the yeast endogenous reductase (Fig. 7A). Shortening of this noncoding sequence to 6 bp in vector pYES2/PsoCPRII resulted in 9-fold greater enzyme activity than in the control yeast strain containing only the vector pYES2. Expression using the integrative yeast vector pRS405 was also investigated for the eventual possible
10 heterologous co-expression of both a plant cytochrome P-450 reductase and a plant oxidase in yeast. Expression of the vector pRS405/PsoCPRII, in which transcription of the *P. somniferum* cytochrome P-450 reductase was also driven by the *GAL1* gene promoter, resulted in 67% of the enzyme activity compared to the autonomously replicating vector pYES2/PsoCPRII.

15 Expression of pYES2/EcaCPRII and of pRS405/EcaCPRII resulted in a 15-fold and 10-fold increase in activity over the endogenous yeast reductase, respectively (Fig. 7C).

The *P. somniferum* cytochrome P-450 reductase reading frame downstream from the GAL 1 promoter was generated by PCR from pYES2/PsoCPRII. The 2598 bp PCR
20 product was ligated into pCRScript and then excised by digestion with *Not* I and *Sal* I. This 2669 bp *Not* I/*Sal* I fragment was ligated into the *Not* I/*Sal* I digested yeast integrative expression vector pRS405 (Stratagene).

The *E. californica* cytochrome P-450 reductase reading frame downstream from the GAL 1 promoter was introduced into the yeast integrative expression vector pRS405
25 by digestion of pYES2/EcaCPRII with *Pst* I and *Not* I and the 2835 bp fragment was ligated into *Pst* I/*Not* I digested vector. The integrative expression plasmids pRS405/PsoCPRII and pRS405/EcaCPRII were then introduced into the *S. cerevisiae* strain INVSC1 under leucine selection.

Yeast microsomes were isolated according to either (22) or (23) and the presence
30 cytochrome P-450 reductase was measured as the ability to reduce cytochrome *c* (24).

Example 4: Heterologous expression of cytochrome P-450 reductase in *Spodoptera frugiperda* Sf9 cells.

The *P. somniferum* cytochrome P-450 reductase cDNA construct pYES2/PsoCPRII was digested with *Hin* dIII and *Xba* I and the resultant 2096 bp
5 fragment was ligated into *Hin* dIII/*Xba* I digested pGEM-7Zf (+) (Promega). pGEM-7Zf/PsoCPRII was then digested with *Bam* HI and *Xho* I and the 2090 bp fragment was ligated into *Bam* HI/*Xho* I digested pFastBac1 (Life Technologies).

The *E. californica* cytochrome P-450 reductase clone pGEM-T/EcaCPRII was digested with the restriction endonucleases *Sma* I and *Not* I and the 2251 bp fragment
10 was ligated into pFastBac1 that had been digested first with *Bam* HI, then with *Pfu* DNA polymerase to produce blunt ends, and finally with *Not* I. pFastBac/PsoCPRII and pFastBac/EcaCPRII were transposed into baculovirus DNA and then transfected into *Spodoptera frugiperda* Sf9 cells according to the manufacturer's instructions. The insect cells were propagated and the recombinant virus was amplified according to (7).
15 Isolation of insect cell microsomes was performed as published (7) and the cytochrome c reducing activity measured as for the yeast expression.

Heterologous expression in insect cell culture (*S. frugiperda* Sf9 cells) of pFastBac/PsoCPRII produced 4-fold more activity than the insect cell endogenous reductase, representing 40% of the activity produced by pYES2/PsoCPRII in yeast (Fig.
20 7B). Expression of pFastBac/PsoCPRI, the construction containing a 27 bp long 5'-noncoding region, resulted in no measurable enzyme activity above that from the endogenous insect cell reductase.

Expression of pFastBac/EcaCPRII in insect cell culture produced a 10-fold increase in reductase activity (Fig 7D). The overexpression in insect cell culture was
25 54% of that achieved in yeast.

Example 5: Co-expression of cytochrome P-450 reductase and berbaminine synthase in Sf9 cells.

To test for the possible effects of a plant cytochrome P-450 reductase as opposed to either yeast or insect cell reductase, several coexpressions were undertaken.

30 Recombinant baculovirus containing either the *P. somniferum* or *E. californica* cytochrome P-450 cDNA was added simultaneously to *S. frugiperda* Sf9 cells (Gibco-

BRL) with recombinant virus containing the berbaminine synthase (CYP 80) cDNA (7). The oxidase virus was infected at a multiplicity of infection (MOI) of approximately 5 and the amount of reductase virus varied from an MOI from 1-5. The infection were carried out as described in (25).

5 The cytochrome P-450 oxidase that was used in these experiments was the *C-O* phenol coupling enzyme of bisbenzylisoquinoline alkaloid biosynthesis from *B. stolonifera*, berbaminine synthase (7). In the presence of equimolar concentrations of the two substrates (*S*)-*N*-methylecclaurine and (*R*)-*N*-methylecclaurine, the native enzyme produces two products in a ratio of 90:10 (berbaminine (*R,S*-
10 dimer):guattegaumerine (*R,R*-dimer)) that correspond to the ratio of these two alkaloids found in the *Berberis* plant (6). Berbaminine synthase expressed in insect cells produced, however, the dimers *R,S*:*R,R* in a ratio of 15:85 (7). Co-infection of insect cell culture with two baculovirus preparations, one containing berbaminine synthase cDNA and the other containing *E. californica* cytochrome P-450 reductase, in varying ratios
15 resulted in a shift in the ratio of the enzymatic products formed as follows: oxidase:reductase (5:1), *R,S*:*R,R* (29:71); oxidase:reductase (1:1), *R,S*:*R,R* (35:65); oxidase:reductase (1:2), *R,S*:*R,R* (37:63).

 The isolation and functional expression of cDNAs encoding cytochrome P-450 reductases from *E. californica* and *P. somniferum* described above were undertaken to
20 develop suitable heterologous expression systems optimal for the active expression of select cytochrome P-450-dependent oxidases of alkaloid biosynthesis, thus providing a convenient test system. Initial characterization of the cytochrome P-450 reductase from *P. somniferum* indicated that with respect to molecular weight, K_m and pH optimum, the reductase is similar to those characterized from other plant species (9,13,14). The
25 purified reductase resolved into two closely migrating bands on SDS-PAGE, suggesting that isoforms are present in *P. somniferum*. This is similar to the finding that multiple reductase isoforms are present in *Arabidopsis thaliana* (16) and *H. tuberosus*. The presence of isoforms in *P. somniferum* was further supported by amino acid sequence analysis of the purified reductase as compared to the sequence identified through cDNA
30 cloning. In addition, isolation of a cDNA encoding cytochrome P-450 reductase from *E. californica* indicated the presence of two isoforms in this plant species as well. The

presence of at least two genes in each genome was corroborated by genomic DNA gel blot analysis.

The cDNA encoding one cytochrome P-450 reductase isoform from each *P. somniferum* and *E. californica* was functionally expressed in yeast in an autonomously replicating vector and in an integrative vector with transcription under the control of the *GALI* gene promoter. These vector constructions resulted in a 6- to 15-fold increase in reductase activity as compared to the activity from the endogenous yeast reductase alone. Likewise, expression of the reductases in insect cell culture using a baculovirus expression vector produced a 4- to 10-fold increase in reductase activity. Improved heterologous expression was obtained when the 5'- noncoding sequences were completely removed from the cDNAs.

Co-expression of the *Eschscholzia* reductase with the plant oxidase berbaminine synthase (7) in insect cell culture indicated that the amount of plant reductase present exerted an influence on the ratio of the products that were enzymatically formed. A first indication of this effect was shown by reconstitution of purified heterologously expressed berbaminine synthase reconstituted with *Berberis* reductase or with porcine reductase (7). Since it is difficult to standardize the lipids when reductase and oxidase are purified from microsomal membranes originating from different organisms, a co-infection of insect cells with reductase and oxidase is one method by which to avoid the varying effects of lipids. An increasing amount of plant reductase resulted in a shift in the ratio of products formed by berbaminine synthase from *R,S:R,R* in a ratio of 15:85 in the absence of *Eschscholzia* reductase to *R,S:R,R* (37:63) when a two-fold excess of baculovirus containing the *Eschscholzia* reductase was used for the co-infection. These results indicate that the cytochrome P-450 reductase may influence the binding of substrate to berbaminine synthase. Although the FMN, FAD and NADPH-binding domains of cytochrome P-450 reductase have been identified by sequence comparisons with well studied flavoproteins, less is known about the substrate binding sites (27,28). Interaction with the non-physiological substrate cytochrome *c* has been demonstrated by chemical cross-linking (29) and by site-directed mutagenesis (30) to involve an acidic region between amino acid residues 200-220 of rat cytochrome P-450 reductase, but an elucidation of the specific interaction between reductase and cytochrome P-450 has not yet been reported.

Example 6: Transformation of poppy plant cells with nucleotide sequences encoding cytochrome P-450 reductase proteins.

General protocols for transformation of *Papaver somniferum* cell suspensions have been published in the literature and would be known to skilled addressees in the field.

The identification and cloning of genes for cytochrome P-450 reductase enzymes now provides means by which the pathway of alkaloid metabolism can be regulated, specifically by alleviating the rate limiting steps which rely on cytochrome P-450. This in turn provides means of obtaining poppy plants with increased yield of alkaloids.

However, there will be instances where it may be preferable to manipulate the alkaloid metabolism of a poppy plant by suppression of genes encoding the P-450 reductases. The expression in the poppy of the cDNA encoding a P-450 reductase enzyme or part thereof, in an antisense orientation can be used to achieve this such that the expression directs the inhibition of the endogenous cytochrome P-450 reductase gene or homologues. In addition, the cDNA encoding the P-450 reductase enzyme or part thereof could be expressed in the sense orientation to direct the co-suppression of the endogenous cytochrome P-450 reductase gene or homologues. Furthermore, the cloned cDNA sequence can be used to design ribozyme sequences such as the hammerhead or hairpin ribozymes that can be used to suppress the target gene by inactivation of the endogenous cytochrome P-450 reductase gene mRNA. The genes encoding the sense, antisense or ribozymes can be delivered as transgenes stably integrated into the poppy genome or transiently in the form of a viral vector.

Although the invention has been described with reference to specific embodiments, modifications that are within the knowledge of those skilled in the art are also contemplated as being within the scope of the present invention.

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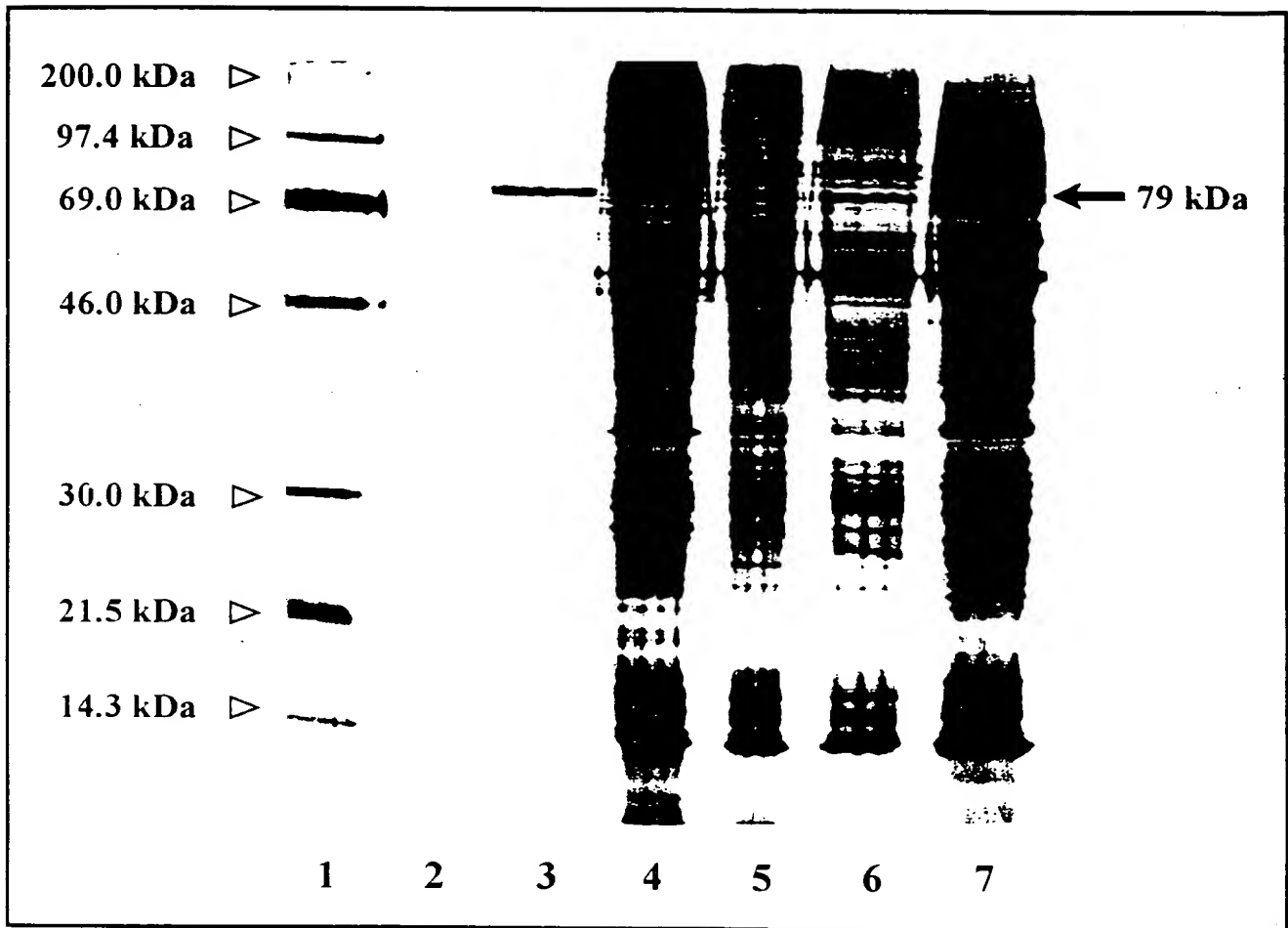


Figure 1.

2/20

Peptide 1 KVTIFFGTQK

Peptide 2 KVVDLDDYAADDDEFEEK
E

Peptide 3 KWFTEVAK
D

Peptide 4 KVVDEIIVEK

Peptide 5 KYADLLNFPK

Peptide 6 KAALHALAK

Peptide 7 KDVHRTLHTIVQEQGLDSSK

Figure 2.

3/20

Arabidopsis thaliana ..350 GSPLES-AVPPPPFPGPCT
Catharanthus roseus ..389 GTPLAGSSLPPPPF-PCT
Helianthus tuberosus ..331 GTPLGGPTLQPPPF-PCT
Vigna radiata ..366 GTSLGG-SLLPPFPGPCS
Vicia sativa ..367 GTSLGG-SLLPPFPGPCT
* . * .. ***** *

LGTGLARYADLLNPPRKSALVALAAYATEPSEA EKLKHLTSPDGKD
LRTALTRYADLLNTPKKSALLALAAYASDPNEADRLKYLASPA GKD
LRKALTNYADLLSSPKKSTLLALA AHASDATEADRLQFLASREGKD
LRTALARYADLLNPPRKAALLALATHASEPS-DE RLKFLSSPQGKD
VRTALACYADLLNPPRKA AIVALAAHASEPSEAERLKFLSSPQGKD
* * ***** * . * . * . * . * . * . *

EYSQWIVASQRSLLEVMAAFPSAKPPLGVFFAAIAPRLQPRYYSIS
EYAQSLVANQRSLLEVMAEFPSAKPPLGVFFAAIAPRLQPRFYSIS
EYAEWIVANQRSLLEVMEAFPSAKPPLGVFFAAIAPRLQPRYYSIS
EYSKWVVG SQRSLEVMAEFPSAKPPLGVFFAAIAPRLQPRYYSIS
EYSKWVVG SQRSLLEVMA DFP SAKPPLGVFFAAIAPRLQPRYYSIS
* . * . * . * . * . * . * . * . * . * . * . *

SCQDWAPSRVHVTSALVYGPTPTGRIHKGVCSTWMKNAVP 498..
SSPRMAPSRIHVTCALVYEKTPGGRIHKGVCSTWMKNAIP 537..
SSPKMVPNRIHVTCALVYEKTPGGRIHKGICSTWMKNAVP 479..
SSPRFAPQRVHVTCALVYGPTPTGRIHKGVCSTWMKNAIP 513..
SSPRPAPQRVHVTCALVEGPTPTGRIHKGVCSTWMKSATP 515..
* . * * . * . * . * . * . * . * . * . * . *

Figure 3.

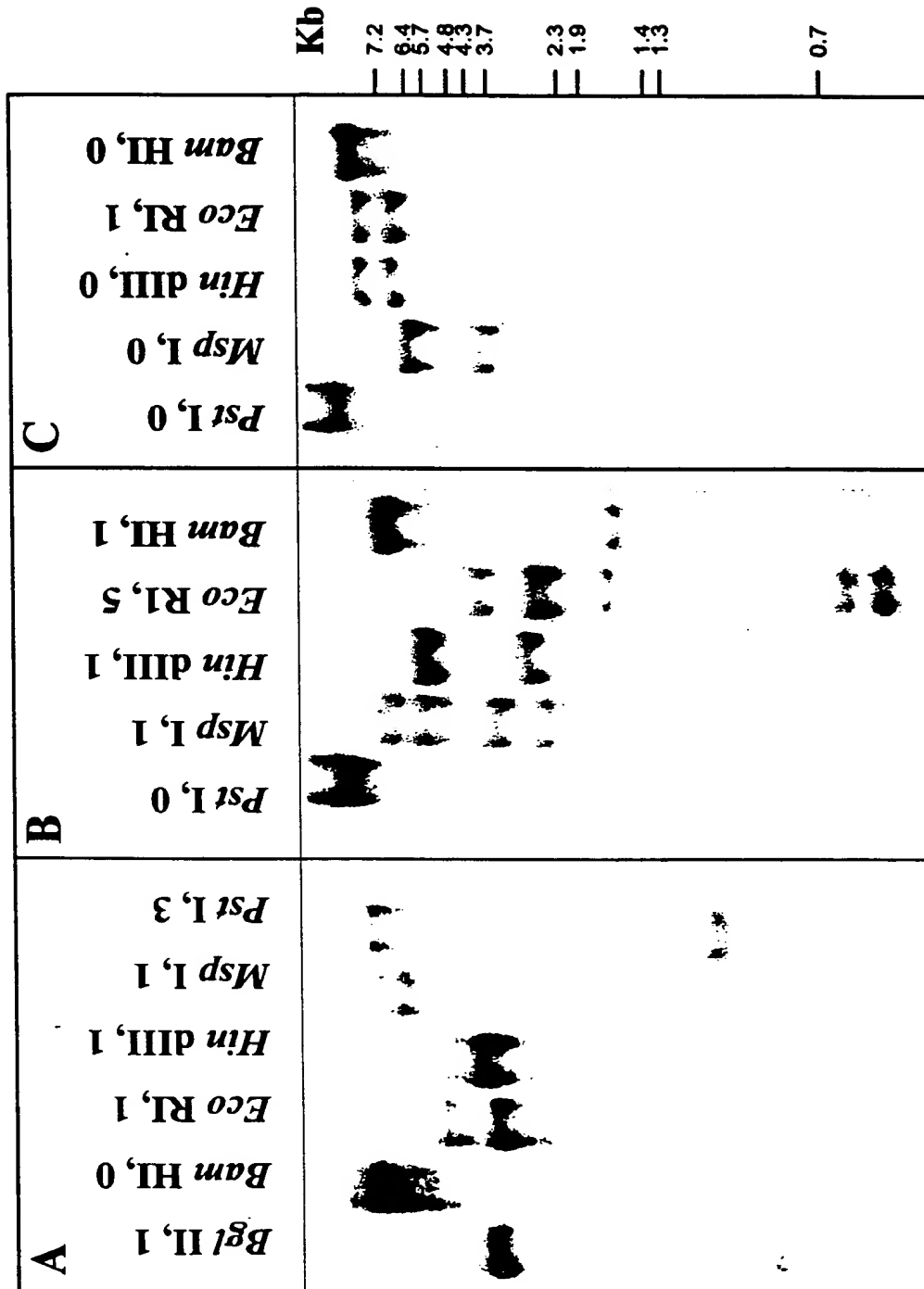


Figure 4.


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1
MEQTAVKVSL FDLFSSILNG KLDPSNFSSD SSAAILIENR EILMILTTAI 50
MGSNNLANSI ESMLG.ISIG ....SEYISD P..... .IFIMVTTVA
* * * * * * * *
51 100
AVFIGCGFLY VWRSSNKSS KIVETQKLIV EKEPE.PEVD DGKKKVTIFF
SMLIGFGFFV CMK.SSSSQS KPIETYKPII DKEEEEIEVD PGKIKLTIFF
** ** * * * * * * * *
101 150
GTQTGTAEFG AKALAEBAKA RYEKAIFKVI DLDDYGADDD EFEEKLKKET
GTQTGTAEFG AKALAEIKA KYKKAVVKVV DLDDYAAEDD QYEEKLKKES
***** ** * * * * * *
151 200
IALFFLATYG DGEPTDNAAR FYKWFTEGKE REMWLQNLQF GVFGGLGNRQY
LVFFMVATYG DGEPTDNAAR FYKWFTQEHE RGEWLQQLTY GVFGGLGNRQY
* **** * * * * * *
201 250
EHFNKVAKEV DEILTEQGGK RIVPVGLGDD DQCIEDDFTA WRELVWPELD
EHFNKIAVDV DEQLGKQGAK RIVQVGLGDD DQCIEDDFTA WRELLWTELD
***** * * * * * * *
251 300
QLLLDESDKT SVSTPYTAIV PEYRVVFHDA TDASLQDKNW SNANGYTVYD
QLLKDEDAAP SVATPYIATV PEYRVVIHET TVAALDDKHI NTANGDVAFD
*** ** * * * * * *
301 350
VQHPCRVV VKKELHTPVVS DRSCIHLEFD ISGTGLTYET GDHVGVSSEN
ILHPCRTIVA QQRELHKPKS DRSCIHLEFD ISGSSLTYET GDHVGVSSEN
**** * * * * * *
351 400
CUEVVEEAER LLGYSSDTVF SIHVDKEDGS PISGSALAPP FPTPCTLRTA
CDETVEEAGK LLGQPLDLLF SIHTDKEDGS PQGSS..LPP FPGPCTLRSA
* * **** * * * * * *
401 450
LTRYADLLNS PKKAALHALA AYASDPKEAE RLRYLASPAG KDEYAQWIVA
LARYADLLNP PRKASLIALS AHASVPSEAE RLRFLSSPLG KNEYSKWVVG
* * * * * * * *
451 500
SQRSLLVMA EFPSAKAPIG VFFAAVAPRL LPRYYSISSS NRMVPSRIHV
SQRSLLLEIMA EFPSAKPPLG VFFAAVAPRL PPRYYSISSS PKFAPSRIHV
***** ** * * * * * *
501 550
TCALVHEKTP AGRVHKGVC S TWMKNSVSLE ENHDCSSWAP IFVRQSNFKL
TCALVYGQSP TGRFHRGVCS TWMKHAVPQD S.....WAP IFVRTSNFKL
***** * * * * * * *
551 600
PADSTVPIIM IGPGTGLAPF RGFMQERLAL KNSGVELGPA ILFFGCRNRQ
PADPSTPIIM VGPGTGLAPF RGFLQERMAL KENGAQLGPA VLFFGCRNRN
*** **** * * * * * *
601 650
MDYIYEEELN NFVKEGAISE VVAFSREGA TKEYVQHKMA EKASYIWEMI
MDFIYEDELN NFVERGVISE LVIAFSREGE KKEYVQHKMM EKATDVWVNI
** * * * * * *
651 700
SQGAYLYVCG DAKGMARDVH RTLHTIAQEQ GSLDNSKTES LVKNLQMDGR
SGDGYLYVCG DAKGMARDVH RTLHTIAQEQ GSMESSAAEA AVKKLQVEER
* * * * * *
701
YLRDVW
YLRDVW
*****

```

Figure 5.

CGGCACGAGCTTGTAGTATCTCTAGGGTTTGAAGGAGCAGGGAGGAGCAAGTGAATCTACTTGAAATACAT
TCGATTGCTTCTCTGTTTAAGCTTCAGAGTCTCTGCTAATATATGGGTTTGAATTAATTAGCTAATTCGATTGAATCGA
TGTTAGGAATATCAATAGGATCAGAAATATAATCTGACCCCAATTTTCAATATGGTCACAACTGTAGCTTCAATGCTGATT
GGATTTGGTTTCTTCGCATGTATGAAAATCTTCGTCTTCTCAATCAAAACCTATTGAAACCTATAAAACCAATAATTGATAA
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GATTTGCTAAGGCATTTGGCAGAGAAAATTAAGGCAAGTACAAGAAAGCAGTTGTTAAAGTAGTTGACCTGGATGACTAT
GCAGCCGAGGATGATCAATATGAAGAGAAAATTAAGAAAGAGTCTTTGGTGTTTTTCATGGTAGCCACTTATGGTGATGG
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CTTATGGTGTTTTGGTTTGGGTAACCGTCAATACGAGCATTTCAACAAGATCGCGGTAGATGTGGATGAGCAACTCGGT
AAACAAGGTGCAAAAGCGCATTTCTCAAGTGGGCTCGGTGACGATGATCAATGCATTTGAAGATGATTTTACTGCTTGGCG
AGAAATGTTGTGGACTGAATTTGGATCAGTTGCTCAAGATGAGGATGCTGCTCCTTCAGTGGCTACACCGTATATTTGCTA
CTGTTCTGAATACAGGGTAGTGATTCACGAAACTACGGTCGCGGCTCTGGATGATAAACACATAAATACTGCTAACGGC
GATGTTGCATTTGATATTTCTCCATCCTTGCAGAACCATTTGTTGCTCAACAAGAGAGCTCCACAAACCCAAAGTCTGATAG
ATCCTGTATACATCTGGAGTTTCCGACATATCAGGCTCTTCCCTTACATATGAGACTGGAGATCATGTTGGTGTATGCTG
AGAACTGCGATGAAACTGTGAGGAAGCAGGGAAGCTGTTGGTCAACCCCTGGATTTGCTGTTTCAATTCACACGGAT
AAAGAAGACGGGTCAACCCAGGGAAGCTCATTAACACCTCCTTTCCAGGTCCTTGCACCTTACGATCTGCCCTAGCACG
CTATGCTGATCTTTGAATCCTCCTAGAAAGGCTTCTCTGATTTGCTCTGCTCGCTCATGCATCTGTACCCAGTGAAGCAG
AGAGATTGCGCTTTTGTCTACACCTCTGGGAAAGAAATGAGTATTCAAAATGGGTAGTTGGAAGTCAGAGGAGTCTTTTG
GAGATCATGGCCGAGTTTCCATCAGCAAAACCCCTCTTGGTGTCTTCTTGTGCTGAGTAGCCCTCGCTTACCGCCTCG
ATACTATTCTATCTCCTCCTAAAGTTTGTCTCCTCAAGAAATTCATGTGACGTGTGCTTTAGTATATGGTCAAAAGCC
CTACCGGAAGGTTTCAACGAGGAGTGTGTTTCGACATGGATGAAGCATGCAGTTCTTCAGGATAGCTGGGCTCCTATTTT
GTTTCAGAGGATTTCTGCAGGAAGAAATGGCCCTCAAGGAAATGGTGTCAACTTGGCCCGCAGCAGTGTCTTTTTCGGAT
GTAGGAATCGTAATATGGACTTCAATTAAGAAGCAACTAAACAACTTCGTGGAAACGAGGAGTAATTTTCGGAGCTAGTT
ATTGCCCTTTTACGTTGAAGGGGAAAGAAAGAAATATGTTCAACATAAGATGATGGAGAAAGCAACGGATGTATGGAATGT
GATATCAGGGGACGGTTATCTCTATGTGTGTGATGCCAAGGGAATGGCCAGAGATGTCCAACGGACGTTGCATACCA
TTGCCCAAGAAACAGGGACCCCATGGAATCATCTGCTGCCAAGCTGCAGTAAAGAAACTCCAAGTTGAAGAACGATATCTA
AGAGATGTCTGGTATCGAATGTAGCTTGCCAAAGTCCCCCTTTTCTTGGCTGGTCTGTTATGGTCTTCTATTAATATTG
ATCCTCCTCTGAAAATCCCAAGCACTTCCAGACATCCCTCGATTTCTCCTCAGTGGTTCCAAATCGAAGCTCGGTATAA
TTGAGAGCAGTGCAATTTGTGACTACATGAGAAAGCAACATCGAATACCATAGAAATTAGAAAGATCAAAATTTCTTTATCA
GAACAAATGTTACAGGCAAAACTGTGTTTGTCTTAATAATAAAATTCACACCAATGGGTGTGGACAACACTGAACAGTATTAG
CTATACCAACAAAGTTATGCAAGGAAACCAAACTAGTTAGATCTTCTCTTTGGATTGATTACTGTAGTTCTTAACCCAGA
TGATAGATTGTACTTAAAGATTCTTTGTTTCTTATGGCTACCGAGAGGAGTATATTAATGCAATTTAGAGTTTGAAGAAAAA

[illegible]

Figure 6b.

Heterologous Expression of P-450 Reductases

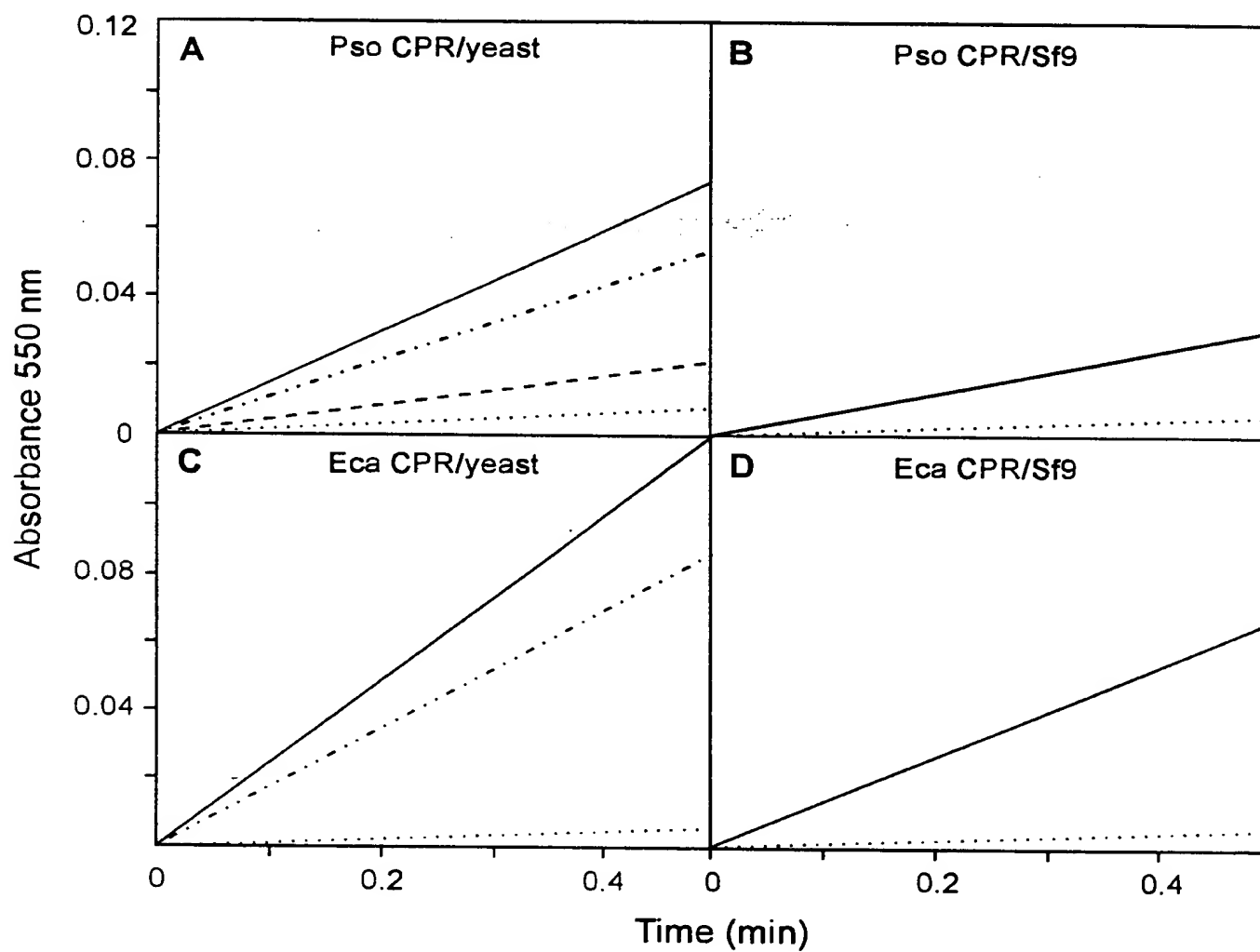


Figure 7.

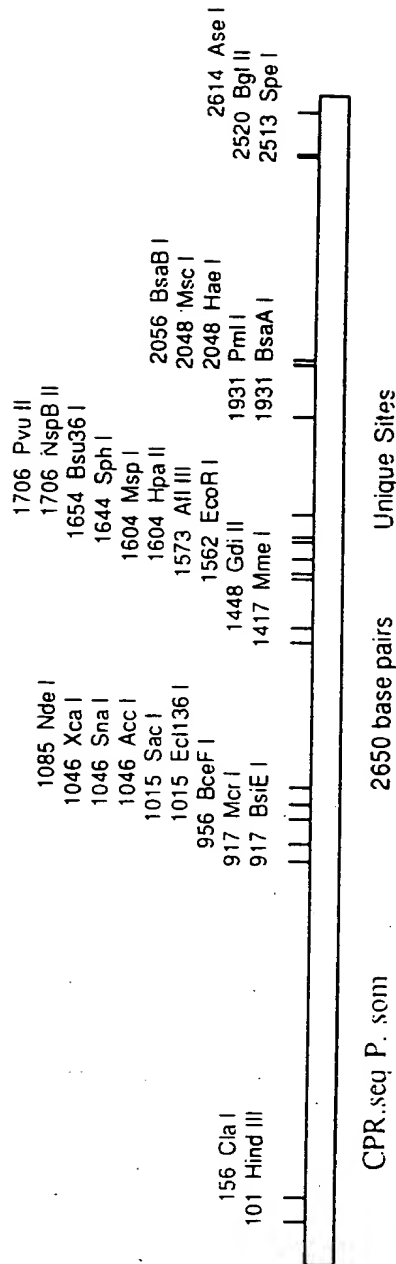


Figure 8a.

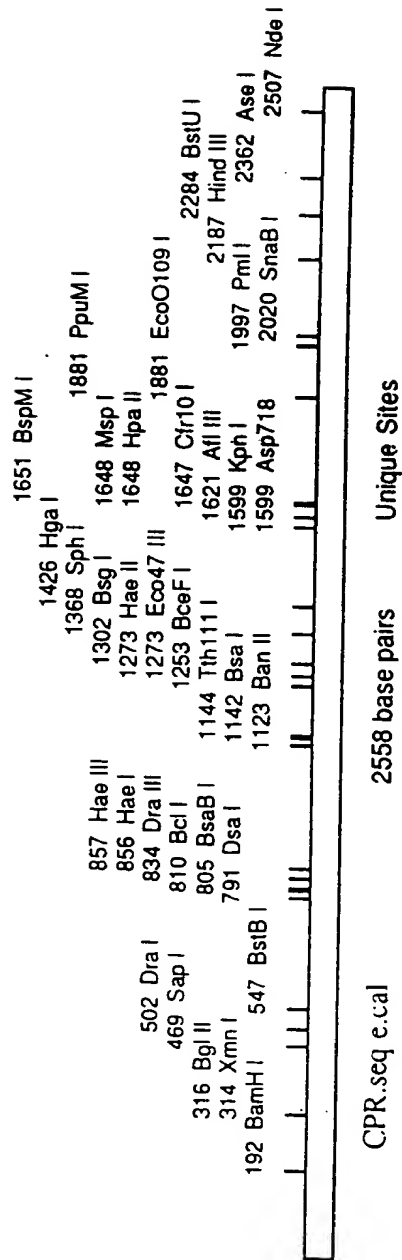


Figure 8b.

1/1	CGG CAC GAG CTT GTT AGT ATC TTC TAG GGT	31/11	TTG AAA AGA AGC ACA GGG AGA AGC AAA AGT
	R H E L V S I F * G		L K R S T G R S K S
61/21	CGA ATC TAC TTG AAA TAC ATT CGA TTG CTT	91/31	CTC TCT GTT TAA GCT TCA GAG TCT CTG CTA
	R I Y L K Y I R L L		L S V * A S E S L L
121/41	ATT ATG GGT TCG AAT AAT TTA GCT AAT TCG	151/51	ATT GAA TCG ATG TTA GGA ATA TCA ATA GGA
	I M G S N N L A N S		I E S M L G I S I G
181/61	TCA GAA TAT ATT TCT GAC CCA ATT TTC ATT	211/71	ATG GTC ACA ACT GTA GCT TCA ATG CTG ATT
	S E Y I S D P I F I		M V T T V A S M L I
241/81	GGA TTT GGT TTC TTC GCA TGT ATG AAA TCT	271/91	TCG TCT TCT CAA TCA AAA CCT ATT GAA ACT
	G F G F F A C M K S		S S S Q S K P I E T
301/101	TAT AAA CCA ATA ATT GAT AAA GAA GAA GAG	331/111	GAG ATT GAA GTT GAT CCT GGT AAA ATT AAG
	Y K P I I D K E E E		E I E V D P G K I K
361/121	CTC ACT ATA TTT TTT GGT ACT CAG ACT GGT	391/131	ACT GCT GAA GGA TTT GCT AAG GCA TTG GCA
	L T I F F G T Q T G		T A E G F A K A L A
421/141	GAA GAA ATT AAG GCA AAG TAC AAG AAA GCA	451/151	GTT GTT AAA GTA GTT GAC CTG GAT GAC TAT
	E E I K A K Y K K A		V V K V V D L D D Y
481/161	GCA GCC GAG GAT GAT CAA TAT GAA GAG AAA	511/171	TTA AAG AAA GAG TCT TTG GTG TTT TTC ATG
	A A E D D Q Y E E K		L K K E S L V F F M
541/181	GTA GCC ACT TAT GGT GAT GGT GAG CCA ACT	571/191	GAC AAT GCT GCG AGA TTT TAC AAA TGG TTC
	V A T Y G D G E P T		D N A A R F Y K W F
601/201	ACT CAG GAA CAT GAA AGG GGA GAG TGG CTT	631/211	CAG CAA CTA ACT TAT GGT GTT TTT GGT TTG
	T Q E H E R G E W L		Q Q L T Y G V F G L
661/221	GGT AAC CGT CAA TAC GAG CAT TTC AAC AAG	691/231	ATC GCG GTA GAT GTG GAT GAG CAA CTC GGT
	G N R Q Y E H F N K		I A V D V D E Q L G
721/241	AAA CAA GGT GCA AAG CGC ATT GTT CAA GTG	751/251	GGG CTC GGT GAC GAT GAT CAA TGC ATT GAA
	K Q G A K R I V Q V		G L G D D D Q C I E
781/261	GAT GAT TTT ACT GCT TGG CGA GAA TTG TTG	811/271	TGG ACT GAA TTG GAT CAG TTG CTC AAA GAT
	D D F T A W R E L L		W T E L D Q L L K D
841/281	GAG GAT GCT GCT CCT TCA GTG GCT ACA CCG	871/291	TAT ATT GCT ACT GTT CCT GAA TAC AGG GTA
	E D A A P S V A T P		Y I A T V P E Y R V
901/301	GTG ATT CAC GAA ACT ACG GTC GCG GCT CTG	931/311	GAT GAT AAA CAC ATA AAT ACT GCT AAC GGC
	V I H E T T V A A L		D D K H I N T A N G
961/321	GAT GTT GCA TTT GAT ATT CTC CAT CCT TGC	991/331	AGA ACC ATT GTT GCT CAA CAA AGA GAG CTC
	D V A F D I L H P C		R T I V A Q Q R E L
1021/341		1051/351	

Figure 9a.

p0A - p0C.

12/20

CAC AAA CCC AAG TCT GAT AGA TCC TGT ATA CAT CTG GAG TTC GAC ATA TCA GGC TCT TCC	
H K P K S D R S C I H L E F D I S G S S	
1081/361	1111/371
CTT ACA TAT GAG ACT GGA GAT CAT GTT GGT GTT TAT GCT GAG AAC TGC GAT GAA ACT GTC	
L T Y E T G D H V G V Y A E N C D E T V	
1141/381	1171/391
GAG GAA GCA GGG AAG CTG TTG GGT CAA CCC CTG GAT TTG CTG TTT TCA ATT CAC ACG GAT	
E E A G K L L G Q P L D L L F S I H T D	
1201/401	1231/411
AAA GAA GAC GGG TCA CCC CAG GGA AGC TCA TTA CCA CCT CCT TTC CCA GGT CCT TGC ACC	
K E D G S P Q G S S L P P P F P G P C T	
1261/421	1291/431
TTA CGA TCT GCC CTA GCA CGC TAT GCT GAT CTT TTG AAT CCT CCT AGA AAG GCT TCT CTG	
L R S A L A R Y A D L L N P P R K A S L	
1321/441	1351/451
ATT GCT CTG TCC GCT CAT GCA TCT GTA CCC AGT GAA GCA GAG AGA TTG CGC TTT TTG TCA	
I A L S A H A S V P S E A E R L R F L S	
1381/461	1411/471
TCA CCT CTG GGA AAG AAT GAG TAT TCA AAA TGG GTA GTT GGA AGT CAG AGG AGT CTT TTG	
S P L G K N E Y S K W V V G S Q R S L L	
1441/481	1471/491
GAG ATC ATG GCC GAG TTT CCA TCA GCA AAA CCC CCT CTT GGT GTT TTC TTT GCT GCA GTA	
E I M A E F P S A K P P L G V F F A A V	
1501/501	1531/511
GCC CCT CGC TTA CCG CCT CGA TAC TAT TCT ATC TCA TCC TCT CCT AAG TTT GCT CCC TCA	
A P R L P P R Y Y S I S S S P K F A P S	
1561/521	1591/531
AGA ATT CAT GTG ACG TGT GCT TTA GTA TAT GGT CAA AGC CCT ACC GGA AGG GTT CAC CGA	
R I H V T C A L V Y G Q S P T G R V H R	
1621/541	1651/551
GGA GTG TGT TCG ACA TGG ATG AAG CAT GCA GTT CCT CAG GAT AGC TGG GCT CCT ATT TTT	
G V C S T W M K H A V P Q D S W A P I F	
1681/561	1711/571
GTT CGA ACG TCA AAC TTC AAG TTA CCA GCT GAC CCC TCA ACT CCA ATT ATC ATG GTG GGA	
V R T S N F K L P A D P S T P I I M V G	
1741/581	1771/591
CCT GGT ACA GGG TTA GCT CCT TTC AGA GGA TTT CTG CAG GAA AGA ATG GCC CTC AAG GAA	
P G T G L A P F R G F L Q E R M A L K E	
1801/601	1831/611
AAT GGT GCT CAA CTT GGC CCA GCA GTG CTC TTT TTC GGA TGT AGG AAT CGT AAT ATG GAC	
N G A Q L G P A V L F F G C R N R N M D	
1861/621	1891/631
TTC ATT TAT GAA GAC GAA CTA AAC AAC TTC GTG GAA CGA GGA GTA ATT TCG GAG CTA GTT	
F I Y E D E L N N F V E R G V I S E L V	
1921/641	1951/651
ATT GCC TTT TCA CGT GAA GGG GAA AAG AAG GAA TAT GTT CAA CAT AAG ATG ATG GAG AAA	
I A F S R E G E K K E Y V Q H K M M E K	
1981/661	2011/671
GCA ACG GAT GTA TGG AAT GTG ATA TCA GGG GAC GGT TAT CTC TAT GTG TGT GGT GAT GCC	
A T D V W N V I S G D G Y L Y V C G D A	
2041/681	2071/691

Figure 9a (cont.).

AAG GGA ATG GCC AGA GAT GTC CAT CGC ACG TTG CAT ACC ATT GCC CAA GAA CAG GGA CCC
 K G M A R D V H R T L H T I A Q E Q G P
 2101/701 2131/711
 ATG GAA TCA TCT GCT GCC GAA GCT GCA GTA AAG AAA CTC CAA GTT GAA GAA CGA TAT CTA
 M E S S A A E A A V K K L Q V E E R Y L
 2161/721 2191/731
 AGA GAT GTC TGG TGA TCG AAT GTA GCT TGC CAA GTC CCC TTT TCT TGG CTG GTC TGT TTA
 R D V W * S N V A C Q V P F S W L V C L
 2221/741 2251/751
 TGG TTT CTA TTA TAT TAT TGA TCC TCC TCT GAA AAT CCC AAG CAC TTC CAG ACA TCC CTC
 W F L L Y Y * S S S E N P K H F Q T S L
 2281/761 2311/771
 GAT TCT TCC TCC AGT GGT TCC AAA TCG AAG CTC GGT ATA ATT GAG AGC AGT GCA ATT GTG
 D S S S S G S K S K L G I I E S S A I V
 2341/781 2371/791
 ACT ACA TGA GAA GCA AAC ATC GAA TAC CAT AGA ATT AGA AAG ATC AAA ATT CTC TTA TCA
 T T * E A N I E Y H R I R K I K I L L S
 2401/801 2431/811
 GAA CAA TGT TAC AGG CAA AAC TGT GTT TGC TTA ATA TAA ATT TCA CAC CAT GGG TGT GGA
 E Q C Y R Q N C V C L I * I S H H G C G
 2461/821 2491/831
 CAA CAC TGA AAC AGT ATT AGC TAT ACC AAC AAA GTT ATG CAA GGA AAC ACA AAC TAG TTA
 Q H * N S I S Y T N K V M Q G N T N * L
 2521/841 2551/851
 GAT CTT CTC TTT GGA TTG ATT ACT GTA AGT TCT AAC CAG ATG ATA GAT TGT ACT TAA AGA
 D L L F G L I T V S S N Q M I D C T * R
 2581/861 2611/871
 TTC TTG TTT TCT TAT GGC TAC CGA GAG GAG TAT ATT AAT GCA TTT AGA GTT TTG AGA AAA
 F L F S Y G Y R E E Y I N A F R V L R K
 2641/881
 AAA AAA AAA A
 K K K

Figure 9a (cont.).

14/20

1/1	31/11
TTC TTC TTC CAA TCG CAT TCG AGA AAA TTC	AAT CAT CTT CAA CTT CAG GAA GAA GAA TCA
F F F Q S H S R K F	N H L Q L Q E E E S
61/21	91/31
TCA GAA ACA CTG AAG CTC ATC ATC ATC CTT	GAA ACT TAT CGT CTT TGT TTG ACC TTT TGA
S E T L K L I I I L	E T Y R L C L T F *
121/41	151/51
AAA ACT ATG GAA CAA ACT GCG GTT AAA GTC	TCT TTG TTT GAT CTA TTT TCT TCG ATA CTT
K T M E Q T A V K V	S L F D L F S S I L
181/61	211/71
AAT GGA AAG TTG GAT CCG TCG AAC TTT TCT	TCA GAT TCA AGT GCT GCT ATT TTG ATT GAA
N G K L D P S N F S	S D S S A A I L I E
241/81	271/91
AAT CGT GAG ATT TTA ATG ATC TTA ACA ACT	GCT ATT GCT GTT TTT ATC GGT TGT GGT TTT
N R E I L M I L T T	A I A V F I G C G F
301/101	331/111
CTC TAC GTT TGG AGA AGA TCT TCA AAT AAG	TCG AGT AAA ATT GTT GAA ACT CAG AAA TTG
L Y V W R R S S N K	S S K I V E T Q K L
361/121	391/131
ATC GTT GAA AAG GAA CCA GAA CCT GAA GTT	GAT GAT GGA AAG AAG AAG GTT ACT ATC TTC
I V E K E P E P E V	D D G K K K V T I F
421/141	451/151
TTT GGT ACT CAA ACT GGT ACA GCT GAA GGA	TTC GCA AAG GCA CTT GCT GAA GAA GCA AAA
F G T Q T G T A E G	F A K A L A E E A K
481/161	511/171
GCA AGA TAT GAA AAG GCA ATC TTT AAA GTG	ATT GAT CTG GAT GAT TAC GGA GCA GAT GAT
A R Y E K A I F K V	I D L D D Y G A D D
541/181	571/191
GAT GAA TTC GAA GAG AAA TTG AAA AAG GAA	ACT ATA GCT CTT TTC TTT TTG GCT ACC TAT
D E F E E K L K K E	T I A L F F L A T Y
601/201	631/211
GGA GAT GGT GAA CCT ACA GAT AAT GCT GCA	AGA TTT TAT AAA TGG TTC ACA GAG GGA GAG
G D G E P T D N A A	R F Y K W F T E G E
661/221	691/231
AGG GAA ATG TGG CTC CAG AAT CTT CAA TTT	GGT GTC TTC GGT CTA GGC AAT AGA CAG TAT
R E M W L Q N L Q F	G V F G L G N R Q Y
721/241	751/251
GAG CAT TTC AAT AAG GTG GCA AAG GAG GTG	GAC GAG ATA CTC ACT GAA CAG GGT GGG AAG
E H F N K V A K E V	D E I L T E Q G G K
781/261	811/271
CGT ATT GTT CCC GTG GGT CTA GGA GAT GAT	GAT CAA TGC ATA GAA GAT GAT TTC ACT GCG
R I V P V G L G D D	D Q C I E D D F T A
841/281	871/291
TGG CGG GAG TTG GTA TGG CCT GAA TTG GAT	CAG TTG CTC CTT GAT GAA AGT GAT AAA ACA
W R E L V W P E L D	Q L L L D E S D K T
901/301	931/311
TCT GTT TCT ACT CCT TAC ACT GCC ATC GTA	CCA GAA TAC AGG GTA GTA TTC CAT GAT GCT
S V S T P Y T A I V	P E Y R V V F H D A
961/321	991/331
ACT GAT GCA TCA CTA CAA GAC AAA AAC TGG	AGC AAT GCA AAT GGC TAC ACT GTT TAC GAC
T D A S L Q D K N W	S N A N G Y T V Y D
1021/341	1051/351

Figure 9b.

15/20

GTT CAA CAC CCA TGC AGA GCC AAT GTC GTT GTA AAG AAG GAG CTT CAC ACT CCA GTA TCT	
V Q H P C R A N V V V K K E L H T P V S	
1081/361	1111/371
GAT CGT TCT TGT ATT CAT CTG GAA TTT GAC ATT TCT GGC ACT GGG CTC ACG TAT GAA ACA	
D R S C I H L E F D I S G T G L T Y E T	
1141/381	1171/391
GGA GAC CAT GTC GGT GTT TAC TCT GAG AAT TGT GTT GAA GTT GTC GAG GAA GCA GAG AGG	
G D H V G V Y S E N C V E V V E E A E R	
1201/401	1231/411
CTA TTG GGT TAC TCA TCA GAC ACC GTT TTT TCA ATC CAT GTC GAT AAA GAG GAC GGC TCA	
L L G Y S S D T V F S I H V D K E D G S	
1261/421	1291/431
CCC ATT AGT GGA AGC GCT CTA GCT CCT CCT TTT CCA ACT CCC TGC ACT CTA AGA ACA GCA	
P I S G S A L A P P F P T P C T L R T A	
1321/441	1351/451
CTA ACA CGA TAC GCT GAT CTG TTG AAT TCT CCC AAG AAG GCT GCT CTG CAT GCT TTG GCT	
L T R Y A D L L N S P K K A A L H A L A	
1381/461	1411/471
GCT TAT GCA TCC GAT CCA AAG GAA GCG GAG CGA CTA AGG TAT CTT GCG TCT CCT GCT GGG	
A Y A S D P K E A E R L R Y L A S P A G	
1441/481	1471/491
AAG GAC GAA TAC GCC CAG TGG ATA GTA GCT AGT CAG AGA AGT CTG CTA GTG GTC ATG GCT	
K D E Y A Q W I V A S Q R S L L V V M A	
1501/501	1531/511
GAA TTC CCA TCA GCA AAG GCT CCA ATT GGG GTT TTC TTT GCA GCA GTA GCT CCT CGC TTG	
E F P S A K A P I G V F F A A V A P R L	
1561/521	1591/531
CTG CCA AGA TAC TAT TCT ATT TCA TCT TCC AAT AGG ATG GTA CCA TCT AGG ATT CAT GTC	
L P R Y Y S I S S S N R M V P S R I H V	
1621/541	1651/551
ACA TGT GCA TTG GTG CAT GAA AAA ACA CCG GCA GGT CGG GTT CAC AAA GGA GTG TGT TCA	
T C A L V H E K T P A G R V H K G V C S	
1681/561	1711/571
ACC TGG ATG AAG AAT TCT GTG TCT TTG GAA GAA AAC CAT GAT TGC AGC AGC TGG GCA CCA	
T W M K N S V S L E E N H D C S S W A P	
1741/581	1771/591
ATC TTT GTC AGG CAA TCC AAC TTC AAA CTT CCT GCT GAT TCT ACA GTA CCA ATT ATA ATG	
I F V R Q S N F K L P A D S T V P I I M	
1801/601	1831/611
ATT GGT CCT GGG ACT GGA TTA GCT CCC TTT AGG GGA TTC ATG CAG GAG CGA TTA GCT CTG	
I G P G T G L A P F R G F M Q E R L A L	
1861/621	1891/631
AAG AAT TCT GGT GTA GAA TTG GGA CCC GCT ATC CTC TTC TTT GGA TGC AGA AAC AGA CAG	
K N S G V E L G P A I L F F G C R N R Q	
1921/641	1951/651
ATG GAT TAC ATA TAT GAA GAG GAG CTA AAC AAC TTT GTG AAA GAG GGA GCT ATC TCC GAA	
M D Y I Y E E E L N N F V K E G A I S E	
1981/661	2011/671
GTT GTT GTT GCT TTC TCA CGT GAG GGA GCT ACC AAG GAA TAC GTA CAA CAT AAA ATG GCG	
V V V A F S R E G A T K E Y V Q H K M A	
2041/681	2071/691

Figure 9b (cont.).

16/20

GAG AAG GCT TCC TAC ATC TGG GAA ATG ATC TCT CAA GGT GCT TAT CTT TAT GTA TGT GGT	
E K A S Y I W E M I S Q G A Y L Y V C G	
2101/701	2131/711
GAT GCC AAG GGC ATG GCT AGA GAC GTA CAT CGA ACT CTC CAC ACC ATT GCC CAG GAA CAG	
D A K G M A R D V H R T L H T I A Q E Q	
2161/721	2191/731
GGA TCT TTG GAC AAC TCG AAG ACC GAA AGC TTG GTG AAG AAT CTA CAG ATG GAT GGA AGG	
G S L D N S K T E S L V K N L Q M D G R	
2221/741	2251/751
TAT CTA CGT GAT GTG TGG TGA TTG ATT TTT TCA GCA CGG TTA CAA TCT AGC TTC ATC AAA	
Y L R D V W * L I F S A R L Q S S F I K	
2281/761	2311/771
GAA CGC GCT TGA GAA GCA TAA ATC TTA GTT GCA GAG ATG TTG ATT TCA GAA GAA ATG CTT	
E R A * E A * I L V A E M L I S E E M L	
2341/781	2371/791
TAT ATA CTT GAG GTA GCG GAC ATT AAT CCT TTT CTC TCT CTC TAA ACT GTT AAT CCT GTA	
Y I L E V A D I N P F L S L * T V N P V	
2401/801	2431/811
AAA AAG GGA TTG CTG TTT GTG TTT GCT CGC AAT CAA TTA AGT TAT ATT CTT TGG TCT ATG	
K K G L L F V F A R N Q L S Y I L W S M	
2461/821	2491/831
GCA TTC GTT AGA CAA ATA TAT TAA CGA GTT TGT CCG TTA TAT ATG ACA TAT GAA ACA AAA	
A F V R Q I Y * R V C P L Y M T Y E T K	
2521/841	2551/851
GAA CTT CTG TTT GGA GGA AGA GAA AAA AAA AAA AAA AA	
E L L F G G R E K K K K	

Figure 9b (cont.).

1	AAGCTTCAGAGTCTCTGCTAATT	ATG	GGT	TCG	AAT	AAT	TTA	GCT	AAT	TCG	ATT	GAA	TCG	ATG	TTA	65
1		M	G	S	N	N	L	A	N	S	I	E	S	M	L	14
66	GGA ATA TCA ATA GGA TCA GAA TAT ATT TCT GAC CCA ATT TTC ATT ATG GTC ACA ACT GTA	125														
15	G I S I G S E Y I S D P I F I M V T T V	34														
126	GCT TCA ATG CTG ATT GGA TTT GGT TTC TTC GCA TGT ATG AAA TCT TCG TCT TCT CAA TCA	185														
35	A S M L I G F G F F A C M K S S S S Q S	54														
186	AAA CCT ATT GAA ACT TAT AAA CCA ATA ATT GAT AAA GAA GAA GAG GAG ATT GAA GTT GAT	245														
55	K P I E T Y K P I I D K E E E E I E V D	74														
246	CCT GGT AAA ATT AAG CTC ACT ATA TTT TTT GGT ACT CAG ACT GGT ACT GCT GAA GGA TTT	305														
75	P G K I K L T I F F G T Q T G T A E G F	94														
306	GCT AAG GCA TTG GCA GAA GAA ATT AAG GCA AAG TAC AAG AAA GCA GTT GTT AAA GTA GTT	365														
95	A K A L A E E I K A K Y K K A V V K V V	114														
366	GAC CTG GAT GAC TAT GCA GCC GAG GAT GAT CAA TAT GAA GAG AAA TTA AAG AAA GAG TCT	425														
115	D L D D Y A A E D D Q Y E E K L K K E S	134														
426	TTG GTG TTT TTC ATG GTA GCC ACT TAT GGT GAT GGT GAG CCA ACT GAC AAT GCT GCG AGA	485														
135	L V F F M V A T Y G D G E P T D N A A R	154														
486	TTT TAC AAA TGG TTC ACT CAG GAA CAT GAA AGG GGA GAG TGG CTT CAG CAA CTA ACT TAT	545														
155	F Y K W F T Q E H E R G E W L Q Q L T Y	174														
546	GGT GTT TTT GGT TTG GGT AAC CGT CAA TAC GAG CAT TTC AAC AAG ATC GCG GTA GAT GTG	605														
175	G V F G L G N R Q Y E H F N K I A V D V	194														
606	GAT GAG CAA CTC GGT AAA CAA GGT GCA AAG CGC ATT GTT CAA GTG GGG CTC GGT GAC GAT	665														
195	D E Q L G K Q G A K R I V Q V G L G D D	214														
666	GAT CAA TGC ATT GAA GAT GAT TTT ACT GCT TGG CGA GAA TTG TTG TGG ACT GAA TTG GAT	725														
215	D Q C I E D D F T A W R E L L W T E L D	234														
726	CAG TTG CTC AAA GAT GAG GAT GCT GCT CCT TCA GTG GCT ACA CCG TAT ATT GCT ACT GTT	785														
235	Q L L K D E D A A P S V A T P Y I A T V	254														
786	CCT GAA TAC AGG GTA GTG ATT CAC GAA ACT ACG GTC GCG GCT CTG GAT GAT AAA CAC ATA	845														
255	P E Y R V V I H E T T V A A L D D K H I	274														
846	AAT ACT GCT AAC GGC GAT GTT GCA TTT GAT ATT CTC CAT CCT TGC AGA ACC ATT GTT GCT	905														
275	N T A N G D V A F D I L H P C R T I V A	294														
906	CAA CAA AGA GAG CTC CAC AAA CCC AAG TCT GAT AGA TCC TGT ATA CAT CTG GAG TTC GAC	965														
295	Q Q R E L H K P K S D R S C I H L E F D	314														
966	ATA TCA GGC TCT TCC CTT ACA TAT GAG ACT GGA GAT CAT GTT GGT GTT TAT GCT GAG AAC	1025														
315	I S G S S L T Y E T G D H V G V Y A E N	334														
1026	TGC GAT GAA ACT GTC GAG GAA GCA GGG AAG CTG TTG GGT CAA CCC CTG GAT TTG CTG TTT	1085														
335	C D E T V E E A G K L L G Q P L D L L F	354														
1086	TCA ATT CAC ACG GAT AAA GAA GAC GGG TCA CCC CAG GGA AGC TCA TTA CCA CCT CCT TTC	1145														
355	S I H T D K E D G S P Q G S S L P P P F	374														

Figure 10a

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1146	CCA	GGT	CCT	TGC	ACC	TTA	CGA	TCT	GCC	CTA	GCA	CGC	TAT	GCT	GAT	CTT	TTG	AAT	CCT	CCT	1205
375	P	G	P	C	T	L	R	S	A	L	A	R	Y	A	D	L	L	N	P	P	394
1206	AGA	AAG	GCT	TCT	CTG	ATT	GCT	CTG	TCC	GCT	CAT	GCA	TCT	GTA	CCC	AGT	GAA	GCA	GAG	AGA	1265
395	R	K	A	S	L	I	A	L	S	A	H	A	S	V	P	S	E	A	E	R	414
1266	TTG	CGC	TTT	TTG	TCA	TCA	CCT	CTG	GGA	AAG	AAT	GAG	TAT	TCA	AAA	TGG	GTA	GTT	GGA	AGT	1325
415	L	R	F	L	S	S	P	L	G	K	N	E	Y	S	K	W	V	V	G	S	434
1326	CAG	AGG	AGT	CTT	TTG	GAG	ATC	ATG	GCC	GAG	TTT	CCA	TCA	GCA	AAA	CCC	CCT	CTT	GGT	GTT	1385
435	Q	R	S	L	L	E	I	M	A	E	F	P	S	A	K	P	P	L	G	V	454
1386	TTC	TTT	GCT	GCA	GTA	GCC	CCT	CGC	TTA	CCG	CCT	CGA	TAC	TAT	TCT	ATC	TCA	TCC	TCT	CCT	1445
455	F	F	A	A	V	A	P	R	L	P	P	R	Y	Y	S	I	S	S	S	P	474
1446	AAG	TTT	GCT	CCC	TCA	AGA	ATT	CAT	GTG	ACG	TGT	GCT	TTA	GTA	TAT	GGT	CAA	AGC	CCT	ACC	1505
475	K	F	A	P	S	R	I	H	V	T	C	A	L	V	Y	G	Q	S	P	T	494
1506	GGA	AGG	GTT	CAC	CGA	GGA	GTG	TGT	TCG	ACA	TGG	ATG	AAG	CAT	GCA	GTT	CCT	CAG	GAT	AGC	1565
495	G	R	V	H	R	G	V	C	S	T	W	M	K	H	A	V	P	Q	D	S	514
1566	TGG	GCT	CCT	ATT	TTT	GTT	CGA	ACG	TCA	AAC	TTC	AAG	TTA	CCA	GCT	GAC	CCC	TCA	ACT	CCA	1625
515	W	A	P	I	F	V	R	T	S	N	F	K	L	P	A	D	P	S	T	P	534
1626	ATT	ATC	ATG	GTG	GGA	CCT	GGT	ACA	GGG	TTA	GCT	CCT	TTC	AGA	GGA	TTT	CTG	CAG	GAA	AGA	1685
535	I	I	M	V	G	P	G	T	G	L	A	P	F	R	G	F	L	Q	E	R	554
1686	ATG	GCC	CTC	AAG	GAA	AAT	GGT	GCT	CAA	CTT	GGC	CCA	GCA	GTG	CTC	TTT	TTC	GGA	TGT	AGG	1745
555	M	A	L	K	E	N	G	A	Q	L	G	P	A	V	L	F	F	G	C	R	574
1746	AAT	CGT	AAT	ATG	GAC	TTC	ATT	TAT	GAA	GAC	GAA	CTA	AAC	AAC	TTC	GTG	GAA	CGA	GGA	GTA	1805
575	N	R	N	M	D	F	I	Y	E	D	E	L	N	N	F	V	E	R	G	V	594
1806	ATT	TCG	GAG	CTA	GTT	ATT	GCC	TTT	TCA	CGT	GAA	GGG	GAA	AAG	AAG	GAA	TAT	GTT	CAA	CAT	1865
595	I	S	E	L	V	I	A	F	S	R	E	G	E	K	K	E	Y	V	Q	H	614
1866	AAG	ATG	ATG	GAG	AAA	GCA	ACG	GAT	GTA	TGG	AAT	GTG	ATA	TCA	GGG	GAC	GGT	TAT	CTC	TAT	1925
615	K	M	M	E	K	A	T	D	V	W	N	V	I	S	G	D	G	Y	L	Y	634
1926	GTG	TGT	GGT	GAT	GCC	AAG	GGA	ATG	GCC	AGA	GAT	GTC	CAT	CGC	ACG	TTG	CAT	ACC	ATT	GCC	1985
635	V	C	G	D	A	K	G	M	A	R	D	V	H	R	T	L	H	T	I	A	654
1986	CAA	GAA	CAG	GGA	CCC	ATG	GAA	TCA	TCT	GCT	GCC	GAA	GCT	GCA	GTA	AAG	AAA	CTC	CAA	GTT	2045
655	Q	E	Q	G	P	M	E	S	S	A	A	E	A	A	V	K	K	L	Q	V	674
2046	GAA	GAA	CGA	TAT	CTA	AGA	GAT	GTC	TGG	TGA	TCGA	ATG	TAG	CTTGCCA	Atcactag						2100
675	E	E	R	Y	L	R	D	V	W	*				M	*						2

Figure 10a (cont.).



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1	tcgagcccggggatccgccCT	ATG GAA CAA ACT GCG GTT AAA GTC TCT TTG TTT GAT CTA TTT	64
1		M E Q T A V K V S L F D L F	14
65	TCT TCG ATA CTT AAT GGA AAG TTG GAT CCG TCG AAC TTT TCT TCA GAT TCA AGT GCT GCT	124	
15	S S I L N G K L D P S N F S S D S S A A	34	
125	ATT TTG ATT GAA AAT CGT GAG ATT TTA ATG ATC TTA ACA ACT GCT ATT GCT GTT TTT ATC	184	
35	I L I E N R E I L M I L T T A I A V F I	54	
185	GGT TGT GGT TTT CTC TAC GTT TGG AGA AGA TCT TCA AAT AAG TCG AGT AAA ATT GTT GAA	244	
55	G C G F L Y V W R R S S N K S S K I V E	74	
245	ACT CAG AAA TTG ATC GTT GAA AAG GAA CCA GAA CCT GAA GTT GAT GAT GGA AAG AAG AAG	304	
75	T Q K L I V E K E P E P E V D D G K K K	94	
305	GTT ACT ATC TTC TTT GGT ACT CAA ACT GGT ACA GCT GAA GGA TTC GCA AAG GCA CTT GCT	364	
95	V T I F F G T Q T G T A E G F A K A L A	114	
365	GAA GAA GCA AAA GCA AGA TAT GAA AAG GCA ATC TTT AAA GTG ATT GAT CTG GAT GAT TAC	424	
115	E E A K A R Y E K A I F K V I D L D D Y	134	
425	GGA GCA GAT GAT GAT GAA TTC GAA GAG AAA TTG AAA AAG GAA ACT ATA GCT CTT TTC TTT	484	
135	G A D D D E F E E K L K K E T I A L F F	154	
485	TTG GCT ACC TAT GGA GAT GGT GAA CCT ACA GAT AAT GCT GCA AGA TTT TAT AAA TGG TTC	544	
155	L A T Y G D G E P T D N A A R F Y K W F	174	
545	ACA GAG GGA GAG AGG GAA ATG TGG CTC CAG AAT CTT CAA TTT GGT GTC TTC GGT CTA GGC	604	
175	T E G E R E M W L Q N L Q F G V F G L G	194	
605	AAT AGA CAG TAT GAG CAT TTC AAT AAG GTG GCA AAG GAG GTG GAC GAG ATA CTC ACT GAA	664	
195	N R Q Y E H F N K V A K E V D E I L T E	214	
665	CAG GGT GGG AAG CGT ATT GTT CCC GTG GGT CTA GGA GAT GAT GAT CAA TGC ATA GAA GAT	724	
215	Q G G K R I V P V G L G D D D Q C I E D	234	
725	GAT TTC ACT GCG TGG CGG GAG TTG GTA TGG CCT GAA TTG GAT CAG TTG CTC CTT GAT GAA	784	
235	D F T A W R E L V W P E L D Q L L L D E	254	
785	AGT GAT AAA ACA TCT GTT TCT ACT CCT TAC ACT GCC ATC GTA CCA GAA TAC AGG GTA GTA	844	
255	S D K T S V S T P Y T A I V P E Y R V V	274	
845	TTC CAT GAT GCT ACT GAT GCA TCA CTA CAA GAC AAA AAC TGG AGC AAT GCA AAT GGC TAC	904	
275	F H D A T D A S L Q D K N W S N A N G Y	294	
905	ACT GTT TAC GAC GTT CAA CAC CCA TGC AGA GCC AAT GTC GTT GTA AAG AAG GAG CTT CAC	964	
295	T V Y D V Q H P C R A N V V V K K E L H	314	
965	ACT CCA GTA TCT GAT CGT TCT TGT ATT CAT CTG GAA TTT GAC ATT TCT GGC ACT GGG CTC	1024	
315	T P V S D R S C I H L E F D I S G T G L	334	
1025	ACG TAT GAA ACA GGA GAC CAT GTC GGT GTT TAC TCT GAG AAT TGT GTT GAA GTT GTC GAG	1084	
335	T Y E T G D H V G V Y S E N C V E V V E	354	
1085	GAA GCA GAG AGG CTA TTG GGT TAC TCA TCA GAC ACC GTT TTT TCA ATC CAT GTC GAT AAA	1144	
355	E A E R L L G Y S S D T V F S I H V D K	374	

Figure 10b

1145	GAG	GAC	GGC	TCA	CCC	ATT	AGT	GGA	AGC	GCT	CTA	GCT	CCT	CCT	TTT	CCA	ACT	CCC	TGC	ACT	1204
375	E	D	G	S	P	I	S	G	S	A	L	A	P	P	F	P	T	P	C	T	394
1205	CTA	AGA	ACA	GCA	CTA	ACA	CGA	TAC	GCT	GAT	CTG	TTG	AAT	TCT	CCC	AAG	AAG	GCT	GCT	CTG	1264
395	L	R	T	A	L	T	R	Y	A	D	L	L	N	S	P	K	K	A	A	L	414
1265	CAT	GCT	TTG	GCT	GCT	TAT	GCA	TCC	GAT	CCA	AAG	GAA	GCG	GAG	CGA	CTA	AGG	TAT	CTT	GCG	1324
415	H	A	L	A	A	Y	A	S	D	P	K	E	A	E	R	L	R	Y	L	A	434
1325	TCT	CCT	GCT	GGG	AAG	GAC	GAA	TAC	GCC	CAG	TGG	ATA	GTA	GCT	AGT	CAG	AGA	AGT	CTG	CTA	1384
435	S	P	A	G	K	D	E	Y	A	Q	W	I	V	A	S	Q	R	S	L	L	454
1385	GTG	GTC	ATG	GCT	GAA	TTC	CCA	TCA	GCA	AAG	GCT	CCA	ATT	GGG	GTT	TTC	TTT	GCA	GCA	GTA	1444
455	V	V	M	A	E	F	P	S	A	K	A	P	I	G	V	F	F	A	A	V	474
1445	GCT	CCT	CGC	TTG	CTG	CCA	AGA	TAC	TAT	TCT	ATT	TCA	TCT	TCC	AAT	AGG	ATG	GTA	CCA	TCT	1504
475	A	P	R	L	L	P	R	Y	Y	S	I	S	S	S	N	R	M	V	P	S	494
1505	AGG	ATT	CAT	GTC	ACA	TGT	GCA	TTG	GTG	CAT	GAA	AAA	ACA	CCG	GCA	GGT	CGG	GTT	CAC	AAA	1564
495	R	I	H	V	T	C	A	L	V	H	E	K	T	P	A	G	R	V	H	K	514
1565	GGA	GTG	TGT	TCA	ACC	TGG	ATG	AAG	AAT	TCT	GTG	TCT	TTG	GAA	GAA	AAC	CAT	GAT	TGC	AGC	1624
515	G	V	C	S	T	W	M	K	N	S	V	S	L	E	E	N	H	D	C	S	534
1625	AGC	TGG	GCA	CCA	ATC	TTT	GTC	AGG	CAA	TCC	AAC	TTC	AAA	CTT	CCT	GCT	GAT	TCT	ACA	GTA	1684
535	S	W	A	P	I	F	V	R	Q	S	N	F	K	L	P	A	D	S	T	V	554
1685	CCA	ATT	ATA	ATG	ATT	GGT	CCT	GGG	ACT	GGA	TTA	GCT	CCC	TTT	AGG	GGA	TTC	ATG	CAG	GAG	1744
555	P	I	I	M	I	G	P	G	T	G	L	A	P	F	R	G	F	M	Q	E	574
1745	CGA	TTA	GCT	CTG	AAG	AAT	TCT	GGT	GTA	GAA	TTG	GGA	CCC	GCT	ATC	CTC	TTC	TTT	GGA	TGC	1804
575	R	L	A	L	K	N	S	G	V	E	L	G	P	A	I	L	F	F	G	C	594
1805	AGA	AAC	AGA	CAG	ATG	GAT	TAC	ATA	TAT	GAA	GAG	GAG	CTA	AAC	AAC	TTT	GTG	AAA	GAG	GGA	1864
595	R	N	R	Q	M	D	Y	I	Y	E	E	E	L	N	N	F	V	K	E	G	614
1865	GCT	ATC	TCC	GAA	GTT	GTT	GTT	GCT	TTC	TCA	CGT	GAG	GGA	GCT	ACC	AAG	GAA	TAC	GTA	CAA	1924
615	A	I	S	E	V	V	V	A	F	S	R	E	G	A	T	K	E	Y	V	Q	634
1925	CAT	AAA	ATG	GCG	GAG	AAG	GCT	TCC	TAC	ATC	TGG	GAA	ATG	ATC	TCT	CAA	GGT	GCT	TAT	CTT	1984
635	H	K	M	A	E	K	A	S	Y	I	W	E	M	I	S	Q	G	A	Y	L	654
1985	TAT	GTA	TGT	GGT	GAT	GCC	AAG	GGC	ATG	GCT	AGA	GAC	GTA	CAT	CGA	ACT	CTC	CAC	ACC	ATT	2044
655	Y	V	C	G	D	A	K	G	M	A	R	D	V	H	R	T	L	H	T	I	674
2045	GCC	CAG	GAA	CAG	GGA	TCT	TTG	GAC	AAC	TCG	AAG	ACC	GAA	AGC	TTG	GTG	AAG	AAT	CTA	CAG	2104
675	A	Q	-E	Q	G	S	L	D	N	S	K	T	E	S	L	V	K	N	L	Q	694
2105	ATG	GAT	GGA	AGG	TAT	CTA	CGT	GAT	GTG	TGG	TGA	TTG	ggg	ctag	agc	ggcc					2154
695	M	D	G	R	Y	L	R	D	V	W	*										705

Figure 10b (cont.).